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OM protein - protein search, using sw model

Run on: October 21, 2004, 11:48:04 ; Search time 155 Seconds  
(without alignments)  
1053.044 Million cell updates/sec

Title: US-09-771-956-13

Perfect score: 2385  
Sequence: 1 MSFYSQDYNMDELDEYNN.....GFLNNGIKADLVSLIHLCHM 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 23Sep04.\*  
1: geneseq1980s.\*  
2: geneseq1990s.\*  
3: geneseq2000s.\*  
4: geneseq2001s.\*  
5: geneseq2002s.\*  
6: geneseq2003as.\*  
7: geneseq2003bs.\*  
8: geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 2385  | 100.0       | 455    | 2     | AAR95939 Human Y5 |
| 2          | 2385  | 100.0       | 455    | 2     | AAR95939 Human Y5 |
| 3          | 2385  | 100.0       | 455    | 2     | AAR95939 Human Y5 |
| 4          | 2385  | 100.0       | 455    | 2     | AAR95939 Human Y5 |
| 5          | 2385  | 100.0       | 455    | 2     | AAR95939 Human Y5 |
| 6          | 2385  | 100.0       | 455    | 4     | AAR95939 Human Y5 |
| 7          | 2385  | 100.0       | 455    | 5     | AAR95939 Human Y5 |
| 8          | 2385  | 100.0       | 455    | 5     | AAR95939 Human Y5 |
| 9          | 2385  | 100.0       | 455    | 8     | AAR95939 Human Y5 |
| 10         | 2385  | 100.0       | 455    | 8     | AAR95939 Human Y5 |
| 11         | 2373  | 99.5        | 445    | 4     | AAR95939 Human Y5 |
| 12         | 2330  | 97.7        | 445    | 2     | AAR95939 Human Y5 |
| 13         | 2330  | 97.7        | 445    | 2     | AAR95939 Human Y5 |
| 14         | 2330  | 97.7        | 445    | 2     | AAR95939 Human Y5 |
| 15         | 2330  | 97.7        | 445    | 3     | AAR95939 Human Y5 |
| 16         | 2330  | 97.7        | 445    | 4     | AAR95939 Human Y5 |
| 17         | 2330  | 97.7        | 445    | 4     | AAR95939 Human Y5 |
| 18         | 2330  | 97.7        | 445    | 4     | AAR95939 Human Y5 |
| 19         | 2330  | 97.7        | 445    | 4     | AAR95939 Human Y5 |
| 20         | 2330  | 97.7        | 445    | 4     | AAR95939 Human Y5 |
| 21         | 2330  | 97.7        | 445    | 6     | AAR95939 Human Y5 |
| 22         | 2330  | 97.7        | 445    | 7     | AAR95939 Human Y5 |
| 23         | 2326  | 97.5        | 499    | 4     | AAR95939 Human Y5 |
| 24         | 2326  | 97.5        | 499    | 5     | AAR95939 Human Y5 |
| 25         | 2321  | 97.3        | 445    | 4     | AAR95939 Human Y5 |

|    |        |      |     |   |                   |
|----|--------|------|-----|---|-------------------|
| 26 | 2318   | 97.2 | 445 | 4 | AAR95939 Human Y5 |
| 27 | 2266   | 95.0 | 445 | 3 | AAR95939 Human Y5 |
| 28 | 2262   | 94.8 | 456 | 2 | AAR95939 Human Y5 |
| 29 | 2084.5 | 87.4 | 456 | 2 | AAR95939 Human Y5 |
| 30 | 2084.5 | 87.4 | 456 | 2 | AAR95939 Human Y5 |
| 31 | 2084.5 | 87.4 | 456 | 2 | AAR95939 Human Y5 |
| 32 | 2084.5 | 87.4 | 456 | 2 | AAR95939 Human Y5 |
| 33 | 2084.5 | 87.4 | 456 | 2 | AAR95939 Human Y5 |
| 34 | 2084.5 | 87.4 | 456 | 5 | AAR95939 Human Y5 |
| 35 | 2074.5 | 87.0 | 445 | 2 | AAR95939 Human Y5 |
| 36 | 2074.5 | 87.0 | 445 | 2 | AAR95939 Human Y5 |
| 37 | 2074.5 | 87.0 | 445 | 3 | AAR95939 Human Y5 |
| 38 | 2074   | 87.0 | 466 | 2 | AAR95939 Human Y5 |
| 39 | 2072.5 | 86.9 | 445 | 2 | AAR95939 Human Y5 |
| 40 | 2070   | 86.8 | 466 | 8 | AAR95939 Human Y5 |
| 41 | 2067.5 | 86.7 | 445 | 2 | AAR95939 Human Y5 |
| 42 | 2067.5 | 86.7 | 445 | 2 | AAR95939 Human Y5 |
| 43 | 2030.5 | 85.1 | 499 | 4 | AAR95939 Human Y5 |
| 44 | 2017   | 84.6 | 508 | 4 | AAR95939 Human Y5 |
| 45 | 1671   | 70.1 | 334 | 2 | AAR95939 Human Y5 |

ALIGNMENTS

RESULT 1

AAR95939  
ID AAR95939 standard; protein; 455 AA.

XX AAR95939;

XX 14-OCT-1996 (first entry)

XX Human Y5 receptor.

XX Y5 receptor; atypical neuropeptide Y1 receptor; feeding behavior;

XX G protein-coupled receptor; agonist; antagonist; obesity; bulimia;

XX anorexia; transgenic animal.

XX Homo sapiens.

XX Key

XX Domain

XX Location/Qualifiers

XX 51..77

XX /label= I

XX /note= "transmembrane domain I"

XX 88..110

XX /label= II

XX /note= "transmembrane domain II"

XX 126..147

XX /label= III

XX /note= "transmembrane domain III"

XX 166..187

XX /label= IV

XX /note= "transmembrane domain IV"

XX 220..242

XX /label= V

XX /note= "transmembrane domain V"

XX 380..403

XX /label= VI

XX /note= "transmembrane domain VI"

XX 416..438

XX /label= VII

XX /note= "transmembrane domain VII"

XX WO9616542-A1.

XX 06-JUN-1996.

XX 01-DEC-1995; 95WO-US015646.

XX 02-DEC-1994; 94US-00349025.

XX (SYNA-) SYNAPTIC PHARM CORP.

XX PA

XX Gerald CPG, Walker MW, Branchek T, Weinshank RL;  
 XX WPI: 1996-277371/28.  
 DR N-PSDB; AAT30433.  
 XX Modifying feeding behaviour using Y5 receptor (ant)agonists - increases  
 PT or decreases food consumption, for treatment of e.g. obesity or bulimia.  
 XX Claim 51; Fig 6; 235pp; English.  
 XX Human hippocampal Y5 receptor (AAR95939) was identified as the homologue  
 CC of rat hypothalamic Y5 receptor (AAR95940), isolated as an 'atypical Y1  
 CC receptor'. The receptor belongs to the G protein-coupled receptor  
 CC superfamily. It is encoded by a cDNA clone (see also AAT30433) that was  
 CC isolated from a hippocampus cDNA library using rat Y5 receptor cDNA as  
 CC probe. Recombinant rat Y5 receptor can be produced in prokaryotic or  
 CC eukaryotic (e.g. COS, 293 or Sf9 insect) host cells. It is used to  
 CC identify Y5 ligands (agonists and antagonists) that can be used to treat  
 CC obesity, bulimia or anorexia, and to raise monoclonal antibodies useful  
 CC in detecting Y5 receptor  
 XX Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-236; Indels 0; Gaps 0;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSFYSKQDYNMDELDYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60  
 Db 1 MSFYSKQDYNMDELDYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60  
 QY 61 VSLGFMGNLLILMALMKRQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120  
 Db 61 VSLGFMGNLLILMALMKRQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120  
 QY 121 KVMCHIMPLOCVSVLSTLILISAIYVYHMKIPISNNLTANHGYFLIATVTLGFAI 180  
 Db 121 KVMCHIMPLOCVSVLSTLILISAIYVYHMKIPISNNLTANHGYFLIATVTLGFAI 180  
 QY 181 CSPLPVHSLVLOETFGSALLSSRYLCSVPWSDSYRIATISLLVQYILPLVCLTVS 240  
 Db 181 CSPLPVHSLVLOETFGSALLSSRYLCSVPWSDSYRIATISLLVQYILPLVCLTVS 240  
 QY 241 HTSVCRSISCGLSNKENLEENINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENLEENINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300  
 QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360  
 Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360  
 QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLPHVTTDFDNDNLISNRHFKLVYCIC 420  
 Db 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLPHVTTDFDNDNLISNRHFKLVYCIC 420  
 QY 421 HLLGMWSCCLPILYGLFNGGKADLVSLIHCLHM 455  
 Db 421 HLLGMWSCCLPILYGLFNGGKADLVSLIHCLHM 455

RESULT 2  
 AAW29447  
 ID AAW29447 standard; protein; 455 AA.  
 AC AAW29447;  
 XX (revised)  
 DT 25-MAR-2003  
 DT 26-FEB-1998 (first entry)  
 DE Human hippocampal neuropeptide Y Y5 receptor.  
 XX Hippocampal; neuropeptide Y Y5 receptor; NPY Y5; antagonist;

KW epileptic seizure; migraine; sleep disturbance; prophylaxis;  
 KW eating disorder; quinzolin-2,4-diazirine.  
 XX Homo sapiens;  
 OS W09720822-A1.  
 XX 12-JUN-1997.  
 XX 18-NOV-1996; 96WO-EP005066.  
 XX 01-DEC-1995; 95US-00566027.  
 XX (NOVS) NOVARTIS AG.  
 XX Rueeger H, Schmidlin T, Rigollier P, Yamaguchi Y,  
 PI Tintelnotblomley M, Schilling W, Criscione L;  
 XX NPI; 1997-319712/29.  
 DR N-PSDB; AAT89114.  
 XX Use of new and known quinzolin-2,4-diazirine compounds as NPY Y5  
 PT receptor antagonists - for treating and preventing eating disorders,  
 PT diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,  
 PT migraine, sleep disturbance, etc.  
 XX Disclosure; Page 127-129; 155pp; English.  
 XX The present sequence represents human hippocampal neuropeptide (NP) Y  
 CC receptor subtype Y5, with a pharmacological function associated with for  
 CC example, obesity and eating disorders. The specification relates to a  
 CC method of treatment and prophylaxis of disorders and diseases associated  
 CC with NPY receptor subtype Y5 comprising administering to a warm-  
 CC blooded animal, including man, in need of such treatment a  
 CC therapeutically effective amount of a quinzolin-2,4-diazirine compound.  
 CC These disorders and diseases include e.g. eating disorders, obesity,  
 CC bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss,  
 CC epileptic seizures, migraine, sleep disturbance, pain,  
 CC sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage,  
 CC shock, congestive heart failure, nasal congestion or diarrhoea. (Updated  
 CC on 25-MAR-2003 to correct PI field.)  
 XX Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-236; Indels 0; Gaps 0;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSFYSKQDYNMDELDYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60  
 Db 1 MSFYSKQDYNMDELDYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60  
 QY 61 VSLGFMGNLLILMALMKRQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120  
 Db 61 VSLGFMGNLLILMALMKRQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120  
 QY 121 KVMCHIMPLOCVSVLSTLILISAIYVYHMKIPISNNLTANHGYFLIATVTLGFAI 180  
 Db 121 KVMCHIMPLOCVSVLSTLILISAIYVYHMKIPISNNLTANHGYFLIATVTLGFAI 180  
 QY 181 CSPLPVHSLVLOETFGSALLSSRYLCSVPWSDSYRIATISLLVQYILPLVCLTVS 240  
 Db 181 CSPLPVHSLVLOETFGSALLSSRYLCSVPWSDSYRIATISLLVQYILPLVCLTVS 240  
 QY 241 HTSVCRSISCGLSNKENLEENINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENLEENINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300  
 QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360  
 Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360  
 QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLPHVTTDFDNDNLISNRHFKLVYCIC 420

Db 361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
QY 421 HLLGMSSCCLNPILYGLFNNNGIKADLVSLIHLCHM 455  
Db 421 HLLGMSSCCLNPILYGLFNNNGIKADLVSLIHLCHM 455

RESULT 3  
AAW29413  
ID AAW29413 standard; protein; 455 AA.

XX AAW29413;  
XX 25-MAR-2003 (revised)  
DT 24-FEB-1998 (first entry)  
XX Human hippocampal neuropeptide Y Y5 receptor.  
XX Human hippocampal neuropeptide Y Y5 receptor; NPY Y5; prophylaxis;  
KW bulimia nervosa; diabetes; dyslipidaemia; hypertension; memory loss;  
KW epileptic seizure; migraine; sleep disturbance; pain; depression;  
KW sexual disorder; anxiety; cerebral haemorrhage, shock; diarrhoea;  
KW congestive heart failure; eating disorder; obesity.  
XX Homo sapiens.  
OS  
XX WO9720820-A1.  
XX 12-JUN-1997.  
XX 16-NOV-1996; 96WO-EP005055.  
XX 01-DEC-1995; 95US-00566349.  
XX (NOVS ) NOVARTIS AG.  
XX Rueger H, Schmidlin T, Rigollier P, Yamaguchi Y;  
PI Tintelnotblomley M, Schilling W, Criscione L;  
XX WPI; 1997-319711/29.  
XX N-PSDB; AAT89110.

Use of new and known heteroaryl compounds as NPY Y5-receptor antagonists  
PT - for treating and preventing eating disorders, diabetes, dyslipidaemia,  
PT hypertension, memory loss, epilepsy, migraine, etc.  
XX  
XX Disclosure; Page 76-78; 155pp; English.

XX This sequence represents human hippocampal neuropeptide (NP) Y receptor  
CC subtype Y5, with a pharmacological function associated with for example,  
CC obesity and eating disorders. The specification relates to a method of  
CC treatment and prophylaxis of disorders and diseases associated with  
CC NPY receptor subtype Y5 comprising administering to a warm-blooded  
CC animal, including man, in need of such treatment a therapeutically  
CC effective amount of a new heteroaryl compound. These disorders and  
CC diseases include e.g. eating disorders, obesity, bulimia nervosa,  
CC diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,  
CC migraine, sleep disturbance, pain, sexual/reproductive disorders,  
CC depression, anxiety, cerebral haemorrhage, shock, congestive heart  
CC failure, nasal congestion or diarrhoea. (Updated on 25-MAR-2003 to  
CC correct PI field.)  
XX  
XX Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.2e-236;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDELYYNNKTLATENNNTAATNSDFPWWDDYKSSVDDLOVELIGLYTF 60  
Db 1 MSFYSKQDYNMDELDELYYNNKTLATENNNTAATNSDFPWWDDYKSSVDDLOVELIGLYTF 60

QY 61 VSLIGFMGNLLILMALMKRNOKTTVNFELIGNLAFSDILVLFCSPTLLTSVLLDQWFG 120  
Db 61 VSLIGFMGNLLILMALMKRNOKTTVNFELIGNLAFSDILVLFCSPTLLTSVLLDQWFG 120  
QY 121 KWCHIMPELQCVSVLSTLILISIAIVRYHMKIPISNNLTAHGYELIATVMTLGPFI 180  
Db 121 KWCHIMPELQCVSVLSTLILISIAIVRYHMKIPISNNLTAHGYELIATVMTLGPFI 180  
QY 181 CSPLPVPHSLVLOETFGSALSSRYLVCVSWPSDSVEIAETISILAVOYILPLVCLTVS 240  
Db 181 CSPLPVPHSLVLOETFGSALSSRYLVCVSWPSDSVEIAETISILAVOYILPLVCLTVS 240  
QY 241 HTSVCRSISCGLSNKENLEENEMINLTHPSKSGQVQLSGHKMSYSFIKRRRYS 300  
Db 241 HTSVCRSISCGLSNKENLEENEMINLTHPSKSGQVQLSGHKMSYSFIKRRRYS 300  
QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSRFIPGVPTCFEIKSEENS DVHEL 360  
Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSRFIPGVPTCFEIKSEENS DVHEL 360  
QY 361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
Db 361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
QY 421 HLLGMSSCCLNPILYGLFNNNGIKADLVSLIHLCHM 455  
Db 421 HLLGMSSCCLNPILYGLFNNNGIKADLVSLIHLCHM 455

RESULT 4  
AAW37093  
ID AAW37093 standard; protein; 455 AA.

XX AAW37093;  
XX 08-JUN-1998 (first entry)  
XX Homo sapiens hippocampal Y5 receptor.  
DE  
XX Hippocampal Y5 receptor; treatment; anorexia; bulimia; obesity;  
KW feeding behaviour; modification; atypical neuropeptide.  
XX  
XX Homo sapiens.

XX WO9746250-A1.  
XX 11-DEC-1997.  
XX 04-JUN-1997; 97WO-US009504.  
XX 04-JUN-1996; 96US-00668650.  
XX 21-FEB-1997; 97US-00803600.  
XX (SYNA-) SYNAPTIC PHARM CORP.  
PI Gerald CP, Weinshank RL, Walker MW, Branchek T;  
XX WPI; 1998-051901/05.  
XX N-PSDB; AAV00622.  
XX DNA encoding canine hypothalamic atypical neuro:peptide Y/peptide YY  
XX receptor, Y5 - useful for identification of compounds which are capable  
XX of modifying feeding behaviour.  
XX  
XX Disclosure; Fig 6; 273pp; English.

XX The sequence is that of a hippocampal Y5 receptor (Y5-R). Y5-R can be  
CC used in processes to determine whether a chemical compound specifically  
CC binds to and activates or inhibits a Y5-R by measuring a second messenger  
CC response. The chemical compounds can be used to increase or reduce the  
CC activity of a Y5-R. In particular, inhibitors can be used to treat  
CC obesity and activators can be used to treat anorexia. Antagonists capable  
CC of alleviating (by decreasing the activity of Y5-R) an abnormality can be

CC identified by administering a potential antagonist to a transgenic mammal  
 CC as above, and determining whether the substance alleviates the physical  
 CC and behavioural abnormalities displayed by the transgenic mammal as a  
 CC result of overactivity of a Y5-R. Agonists can be identified in a similar  
 CC manner, but where the abnormality is alleviated by increasing the  
 CC activity of Y5-R  
 XX  
 SQ Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-236;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSQDYNMDELDEYYNKTATENTTAATRNDDFPVMDYKSSVDDLOVFLIGLYTF 60  
 DB 1 MSFYSQDYNMDELDEYYNKTATENTTAATRNDDFPVMDYKSSVDDLOVFLIGLYTF 60

QY 61 VSLGFMGNLLILMALMKRNOKTTVFNFLGNLAFSDILVLFCSPTLTSLVLLDQWVFG 120  
 DB 61 VSLGFMGNLLILMALMKRNOKTTVFNFLGNLAFSDILVLFCSPTLTSLVLLDQWVFG 120

QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPIISNNLTANHGYFLIATVMTLGF 180  
 DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPIISNNLTANHGYFLIATVMTLGF 180

QY 181 CSPLPVFHSVLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
 DB 181 CSPLPVFHSVLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKRRRYS 300  
 DB 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKRRRYS 300

QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPIGVPTCTCFEIKPEENSVDHEL 360  
 DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPIGVPTCTCFEIKPEENSVDHEL 360

QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSWMPLHLFHVTTDFNDNLISNRHFKLVYCIC 420  
 DB 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSWMPLHLFHVTTDFNDNLISNRHFKLVYCIC 420

QY 421 HLLGMWSCCLNPILYGFLLNGIKADLVSLIHCLHM 455  
 DB 421 HLLGMWSCCLNPILYGFLLNGIKADLVSLIHCLHM 455

RESULT 5  
 AAY57461  
 ID AAY57461 standard; protein; 455 AA.  
 XX  
 AC AAY57461;  
 XX  
 DT 25-FEB-2000 (first entry)  
 XX  
 DE Human hippocampal Y5 receptor.  
 XX  
 KW Y5 receptor; feeding behaviour; food consumption; obesity; bulimia;  
 XX anorexia; neuropeptide; genetic engineering.  
 XX Homo sapiens.  
 XX US968819-A.  
 XX 19-OCT-1999.  
 XX 01-DEC-1995; 95US-00566096.  
 XX 02-DEC-1994; 94US-00349025.  
 XX (SYNA-) SYNAPTIC PHARM CORP.  
 XX Walker MW, Branchek T, Gerald CPG, Weinshank RL;  
 XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;  
 XX transmembrane; TM domain; therapy; blood pressure; epilepsy;

DR WPI; 1999-590415/50.  
 DR N-PSDB; AAZ39046.  
 XX  
 PT Nucleic acid encoding a human neuropeptide Y receptor useful in genetic  
 XX engineering.  
 XX  
 PS Disclosure; Fig 6; 87pp; English.

The present sequence represents the human hippocampal Y5 receptor. The Y5  
 receptor is a G-protein coupled neuropeptide Y receptor found throughout  
 the mammalian nervous system and is a powerful stimulant of feeding  
 behaviour. Cells expressing DNA encoding the Y5 receptor can be used to  
 determine whether a ligand specifically binds to a Y5 receptor. These  
 cells or a cell extract, is exposed to the ligand and then any binding  
 between the ligand and the receptor can be detected. The cells can also  
 be used to determine whether a ligand is a Y5 receptor antagonist or  
 agonist. The binding of chemical compounds to a Y5 receptor can also  
 be determined and whether they activate or inhibit the activation of the Y5  
 receptor can also be determined using cells expressing the receptor. The  
 effect of drugs on the Y5 receptor and whether they act as agonists or  
 antagonists can also be detected with these cells

Query Match 100.0%; Score 2385; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-236;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSQDYNMDELDEYYNKTATENTTAATRNDDFPVMDYKSSVDDLOVFLIGLYTF 60  
 DB 1 MSFYSQDYNMDELDEYYNKTATENTTAATRNDDFPVMDYKSSVDDLOVFLIGLYTF 60

QY 61 VSLGFMGNLLILMALMKRNOKTTVFNFLGNLAFSDILVLFCSPTLTSLVLLDQWVFG 120  
 DB 61 VSLGFMGNLLILMALMKRNOKTTVFNFLGNLAFSDILVLFCSPTLTSLVLLDQWVFG 120

QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPIISNNLTANHGYFLIATVMTLGF 180  
 DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPIISNNLTANHGYFLIATVMTLGF 180

QY 181 CSPLPVFHSVLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
 DB 181 CSPLPVFHSVLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKRRRYS 300  
 DB 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKRRRYS 300

QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPIGVPTCTCFEIKPEENSVDHEL 360  
 DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPIGVPTCTCFEIKPEENSVDHEL 360

QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSWMPLHLFHVTTDFNDNLISNRHFKLVYCIC 420  
 DB 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSWMPLHLFHVTTDFNDNLISNRHFKLVYCIC 420

QY 421 HLLGMWSCCLNPILYGFLLNGIKADLVSLIHCLHM 455  
 DB 421 HLLGMWSCCLNPILYGFLLNGIKADLVSLIHCLHM 455

RESULT 6  
 AAE08002  
 ID AAE08002 standard; protein; 455 AA.  
 XX  
 AC AAE08002;  
 XX  
 DT 01-NOV-2001 (first entry)  
 XX  
 DE Human neuropeptide Y5 (NPY5) receptor.  
 XX  
 KW Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;  
 transmembrane; TM domain; therapy; blood pressure; epilepsy;



KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;  
 XX locomotor; anxiety disorder; limbic seizure; tranquilliser; human.  
 OS Homo sapiens.  
 FH Key  
 FT Domain 1. .50  
 FT Domain /note= "N-terminal extracellular domain"  
 FT Domain 51. .71  
 FT Domain /note= "First TM domain"  
 FT Domain 72. .84  
 FT Domain /note= "First intracellular loop domain"  
 FT Domain 85. .105  
 FT Domain /note= "Second TM domain"  
 FT Domain 106. .125  
 FT Domain /note= "First extracellular loop domain"  
 FT Domain 126. .146  
 FT Domain /note= "Third TM domain"  
 FT Domain 147. .167  
 FT Domain /note= "Second intracellular loop domain"  
 FT Domain 168. .188  
 FT Domain /note= "Fourth TM domain"  
 FT Domain 189. .220  
 FT Domain /note= "Second extracellular loop domain"  
 FT Domain 221. .241  
 FT Domain /note= "Fifth TM domain"  
 FT Domain 242. .378  
 FT Domain /note= "Third intracellular loop domain"  
 FT Domain 379. .401  
 FT Domain /note= "Sixth TM domain"  
 FT Domain 402. .414  
 FT Domain /note= "Third extracellular loop domain"  
 FT Domain 415. .438  
 FT Domain /note= "Seventh TM domain"  
 FT Domain 439. .455  
 FT Domain /note= "C-terminal intracellular domain"  
 XX  
 XX WO200155103-A2.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 29-JAN-2001; 2001WO-US002804.  
 XX  
 XX 28-JAN-2000; 2000US-0178652P.  
 XX (NEUR-) NEUROGEN CORP.  
 XX  
 XX Bennett M, Brodbeck R, Krause J;  
 XX  
 XX WPI; 2001-514543/56.  
 XX N-PSDB; AAD14734.  
 XX  
 XX New chimeric receptor proteins comprising a single polypeptide chain of  
 PT amino acids useful as targets for drug actions, and as basis for drug  
 PT discovery and development.  
 XX  
 XX Example 2; Page 55-56; 72pp; English.  
 XX  
 XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.  
 CC The NPY receptors are G-protein-coupled transmembrane proteins with seven  
 CC membrane spanning transmembrane (TM) domains. The compounds that modulate  
 CC the activity of a NPY receptor is useful in the preparation of a  
 CC medicament for treating conditions including obesity, high/low blood  
 CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,  
 CC seizure, locomotor and anxiety disorders. They can also be used as  
 CC targets for drug actions, and as basis for drug discovery and  
 CC development. The NPY5 receptor may have an anti-epileptic activity in the  
 CC control of limbic seizures. The present sequence is human NPY5 receptor  
 XX  
 XX Sequence 455 AA;  
 SQ  
 Query Match 100.0%; Score 2385; DB 4; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-236;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSFYSKQDYNMDELEDEYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60  
 Db 1 MSFYSKQDYNMDELEDEYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60  
 Qy 61 VSLGFGWGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSLVLDQWFG 120  
 Db 61 VSLGFGWGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSLVLDQWFG 120  
 Qy 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKPIENNLTAHGYFLIATVTLGFAI 180  
 Db 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKPIENNLTAHGYFLIATVTLGFAI 180  
 Qy 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
 Db 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
 Qy 241 HTSVCRSISCGLSNKENRLEENEMINLTHPSKSGQVQLSGSHKWSYSIKHHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENRLEENEMINLTHPSKSGQVQLSGSHKWSYSIKHHRRYS 300  
 Qy 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFIKPEENS DVHEL 360  
 Db 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFIKPEENS DVHEL 360  
 Qy 361 RVKRSVTRIKGSRSVFYRLTILILVFAVSMWPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 Db 361 RVKRSVTRIKGSRSVFYRLTILILVFAVSMWPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 Qy 421 HLLGWMSCCLNPILYGFNLNGIKADLVSLIHLHM 455  
 Db 421 HLLGWMSCCLNPILYGFNLNGIKADLVSLIHLHM 455  
 RESULT 7  
 ABB84497  
 ID ABB84497 standard; protein; 455 AA.  
 AC ABB84497;  
 XX  
 XX 20-DEC-2002 (first entry)  
 DT  
 DE Human hippocampus Y5 receptor protein.  
 XX  
 XX Human; hippocampus; Y5; receptor; feeding behaviour; Y5 receptor;  
 KW food consumption; metabolic; anorectic; antidepressant; tranquilliser;  
 KW atinigraine; analgesic; hypotensive; cerebroprotective; cardiant;  
 KW antidarrhoeic; haemostatic; vaccine; anorexia; obesity; bulimia;  
 KW sexual disorder; reproductive disorder; depression; anxiety; memory loss;  
 KW migraine; pain; epileptic seizure; hypertension; cerebral haemorrhage;  
 KW shock; congestive heart failure; sleeve disturbance; nasal congestion;  
 KW diarrhoea.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US2002103123-A1.  
 PN  
 XX 01-AUG-2002.  
 PD  
 XX 24-SEP-2001; 2001US-00962646.  
 XX  
 XX 02-DEC-1994; 94US-00349025.  
 PR 01-DEC-1995; 95US-00566096.  
 PR 25-NOV-1998; 98US-00200673.  
 XX  
 XX (SYNA-) SYNAPTIC PHARM CORP.  
 PA  
 XX Gerald CPG, Weinshank RL, Walker MW, Branchek T;  
 PI  
 XX WPI; 2002-712388/77.  
 DR N-PSDB; AAF88821.  
 XX

PT Modifying feeding behavior of subject, useful in treating feeding disorders, involves administering to subject Y5 receptor agonist or antagonist, to increase or decrease consumption of food by subject.

XX

XX Claim 53; Fig 6; 102pp; English.

XX This invention describes a novel method of modifying feeding behaviour of a subject which involves administering to the subject an amount of a compound which is a Y5 receptor agonist or antagonist effective to increase or decrease, respectively, the consumption of food by the subject so as to modify feeding behaviour of the subject. The product of the invention has metabolic, anorectic, antidepressant, tranquiliser, anti-migraine, analgesic, hypotensive, cerebroprotective, cardiac, anti-diarrhoeic and haemostatic activity and can be used in a vaccine. Y5 receptor agonist or antagonist compounds are useful for treating a feeding disorder (e.g. anorexia, obesity or bulimia) in a subject. The pharmaceutical compositions described in the disclosure are useful for treating an abnormality alleviated by the inhibition or activation of Y5 receptor, in a subject. Antibodies raised against the receptor are useful for detecting the presence of the receptor on the surface of a cell. The agonist of Y5 receptor is useful for treating an abnormality in a subject, where the abnormality includes anorexia, sexual/reproductive disorder, depression, anxiety, memory loss, migraine, pain, epileptic seizure, hypertension, cerebral haemorrhage, shock, congestive heart failure, sleeve disturbance, nasal congestion, and diarrhoea. This sequence represents the human hippocampus Y5 receptor described in the disclosure of the invention

XX

SQ Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 5; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-236;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDYVYKTLATENNNTAATRNSTDFPVDYKSSVDLQYFLGLYTF 60  
 DB 1 MSFYSKQDYNMDELDYVYKTLATENNNTAATRNSTDFPVDYKSSVDLQYFLGLYTF 60

QY 61 VSLGFMGNLLILMALMKRQKTTNFIENLAFSDILVLFCSPTFTSVLLDQWFG 120  
 DB 61 VSLGFMGNLLILMALMKRQKTTNFIENLAFSDILVLFCSPTFTSVLLDQWFG 120

QY 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVTLGFAI 180  
 DB 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVTLGFAI 180

QY 181 CSPLPVPHSLVLOETFGSALLSRYLCSVPSPDSYRIAFITISLLVQYILPLVCLTVS 240  
 DB 181 CSPLPVPHSLVLOETFGSALLSRYLCSVPSPDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENINLTLPSPKSGQVQLSGHKWSYFIKHHRRYS 300  
 DB 241 HTSVCRSISCGLSNKENLEENINLTLPSPKSGQVQLSGHKWSYFIKHHRRYS 300

QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCEIPEENSDVHEL 360  
 DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCEIPEENSDVHEL 360

QY 361 RVKRSVTRIKRSRSVFRILITILVPAVSMPLHLFHVTVDFNDNISNRHFKLVYIC 420  
 DB 361 RVKRSVTRIKRSRSVFRILITILVPAVSMPLHLFHVTVDFNDNISNRHFKLVYIC 420

QY 421 HLLGWMSCCLNPILYGLFNGGKADLVSLIHCLHM 455  
 DB 421 HLLGWMSCCLNPILYGLFNGGKADLVSLIHCLHM 455

RESULT 8  
 ABB79510  
 ID ABB79510 standard; protein; 455 AA.  
 XX  
 AC ABB79510;  
 XX

DT 23-SEP-2002 (first entry)  
 XX Human neurotensin Y5 receptor.  
 DE  
 XX Neurotensin Y5; NPV; NPV5; receptor; human; antagonist; anorectic;  
 KW antiinflammatory; nootropic; neuroprotective; cardiovascular;  
 KW hypotensive; antidiabetic; psychiatric; anticonvulsant; cardiac;  
 KW cerebroprotective; antidepressant; haemostatic; tranquilizer;  
 KW neuroleptic; analgesic; antianginal; nephrotropic; uropathic;  
 KW gastrointestinal; antiasthmatic.  
 OS Homo sapiens.  
 XX WO200248152-A2.  
 PN 20-JUN-2002.  
 XX 11-DEC-2001; 2001WO-US047863.  
 XX 12-DEC-2000; 2000US-0254990P.  
 XX (NEUR-) NEUROGEN CORP.  
 PA Bakthavatchalam R, Blum CA, Brielmann HL, Darrow JW;  
 PI De Lombaert S, Hutchison A, Tran J, Zheng X, Elliott RL, Hammond M;  
 DR WPI: 2002-547845/58.  
 DR N-PSDE; ABN84252.  
 XX New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or 3H-  
 PT spiro(isobenzofuran-1,4'-piperidine, useful for treating, e.g. eating  
 disorder, psychiatric, cardiovascular disorder or diabetes.  
 XX Example 675; Page 129-130; 134pp; English.

The present sequence is the protein sequence for the human neurotensin  
 Y5 (NPV5) receptor. In an example from the invention, chimeric receptors  
 including human NPV5 receptor sequences were constructed, and used to  
 assay the binding activity of compounds of the invention. Substituted  
 spiro(isobenzofuran-1,4'-piperidin)-3-ones and 3H-spiro(isobenzofuran-1,4'-  
 piperidines capable of modulating NPV5 receptor activity are provided.  
 Such compounds may be used to modulate ligand binding to NPV5 receptors  
 in vivo or in vitro, and are particularly useful in the treatment of a  
 variety of disorders, e.g. eating disorders such as obesity or bulimia,  
 psychiatric disorders, diabetes and cardiovascular disorders such as  
 hypertension, in humans and animals

XX Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 5; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-236;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDYVYKTLATENNNTAATRNSTDFPVDYKSSVDLQYFLGLYTF 60  
 DB 1 MSFYSKQDYNMDELDYVYKTLATENNNTAATRNSTDFPVDYKSSVDLQYFLGLYTF 60

QY 61 VSLGFMGNLLILMALMKRQKTTNFIENLAFSDILVLFCSPTFTSVLLDQWFG 120  
 DB 61 VSLGFMGNLLILMALMKRQKTTNFIENLAFSDILVLFCSPTFTSVLLDQWFG 120

QY 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVTLGFAI 180  
 DB 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVTLGFAI 180

QY 181 CSPLPVPHSLVLOETFGSALLSRYLCSVPSPDSYRIAFITISLLVQYILPLVCLTVS 240  
 DB 181 CSPLPVPHSLVLOETFGSALLSRYLCSVPSPDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENINLTLPSPKSGQVQLSGHKWSYFIKHHRRYS 300  
 DB 241 HTSVCRSISCGLSNKENLEENINLTLPSPKSGQVQLSGHKWSYFIKHHRRYS 300

Qy 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFIKPEENSVDHEL 360  
Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFIKPEENSVDHEL 360  
Qy 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYIC 420  
Db 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYIC 420  
Qy 421 HLLGMSCCCLNPILYGLFNNGIKADLVSLIHLHM 455  
Db 421 HLLGMSCCCLNPILYGLFNNGIKADLVSLIHLHM 455

RESULT 9  
AAO23266  
ID AAO23266 standard; protein; 455 AA.  
XX AC AAO23266;  
XX DT 25-SEP-2003 (first entry)  
XX DE Human neuropeptide Y5 receptor (NPY5) protein.

Neuropeptide Y5; receptor; NPY5; 2-cyclohexyl-4-phenyl-1H-imidazole; NPY;  
appetite regulation; feeding disorder; obesity; bulimia; diabetes;  
psychiatric; cardiovascular; hypertension; cerebral infarction; epilepsy;  
schizophrenia; depression; angina; sudden cardiac death; vasospasm;  
arrhythmia; urinary incontinence; Crohn's disease; asthma; neuroleptic;  
antiinflammatory; nootropic; vasotropic; anticonvulsant; uropathic;  
human.

OS Homo sapiens.  
XX PN EPI306085-A1.  
XX PD 02-MAY-2003.  
XX PF 21-OCT-2002; 2002EP-00023469.  
XX PR 23-OCT-2001; 2001US-0348974P.  
XX PA (NEUR-) NEUROGEN CORP.  
XX PI Blum CA, Brielmann HL, De Lombaert S, Zheng X;  
XX DR WPI; 2003-543553/52.  
XX DR N-PSDB; AAL56583.

PT New 2-cyclohexyl-4-phenyl-1H-imidazole derivatives are modulators of  
PT neuropeptide Y5 receptor activity, useful for treating e.g. eating or  
PT psychiatric disorders.  
XX Example 10; Page 39-41; 63pp; English.

XX This invention relates to novel ligands (derivatives of 2-cyclohexyl-4-  
XX phenyl-1H-imidazole) for the neuropeptide Y5 (NPY5) receptor. The NPY5  
XX receptor mediates a variety of physiological effects and is involved in  
XX appetite regulation, hormone release and blood pressure. Ligands that  
XX can be used to treat a variety of conditions including feeding disorders  
XX (obesity and bulimia), psychiatric disorders, diabetes and cardiovascular  
XX diseases such as hypertension. Further uses relate to the treatment of  
XX cerebral infarction, epilepsy, schizophrenia, depression, angina, sudden  
XX cardiac death, vasospasm, arrhythmia, urinary incontinence, Crohn's  
XX disease and asthma. As such these ligands can be described variously as  
XX neuroleptic, antiinflammatory, nootropic, vasotropic, anticonvulsant and  
XX uropathic. This polypeptide sequence is the human neuropeptide Y5 (NPY5)  
XX receptor protein of the invention

XX Sequence 455 AA;  
Query Match 100.0%; Score 2385; DB 6; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.2e-236;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSFYSQDYNMDELDDEYNNKTLATENTTAATRNDDFPVWDYKSSVDDLOVFLGLYTF 60  
Db 1 MSFYSQDYNMDELDDEYNNKTLATENTTAATRNDDFPVWDYKSSVDDLOVFLGLYTF 60  
Qy 61 VSLILGFWGNLLIIMALKMKRNOKTTVNFILIGNLAFSDILVLFQSPFTLTSLVLLDQWFG 120  
Db 61 VSLILGFWGNLLIIMALKMKRNOKTTVNFILIGNLAFSDILVLFQSPFTLTSLVLLDQWFG 120  
Qy 121 KVMCHIMPLOQCVSVLVSTLILISIAIVRYHMIKPIISNNLTANHGYFLIATVWTLGFAI 180  
Db 121 KVMCHIMPLOQCVSVLVSTLILISIAIVRYHMIKPIISNNLTANHGYFLIATVWTLGFAI 180  
Qy 181 CSPLPVFHSILVELQETFGSALLSSRYLCVESWPSDSYRIAPTISILLVQYILPLVCLTVS 240  
Db 181 CSPLPVFHSILVELQETFGSALLSSRYLCVESWPSDSYRIAPTISILLVQYILPLVCLTVS 240  
Qy 241 HTSVCSISICGLSNKENRLEENEMINLTHPSKSGPQVKLSGSHKWSYSIKHHRRYS 300  
Db 241 HTSVCSISICGLSNKENRLEENEMINLTHPSKSGPQVKLSGSHKWSYSIKHHRRYS 300  
Qy 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFIKPEENSVDHEL 360  
Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFIKPEENSVDHEL 360  
Qy 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYIC 420  
Db 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYIC 420  
Qy 421 HLLGMSCCCLNPILYGLFNNGIKADLVSLIHLHM 455  
Db 421 HLLGMSCCCLNPILYGLFNNGIKADLVSLIHLHM 455

RESULT 10  
ADO29564  
ID ADO29564 standard; protein; 455 AA.  
XX AC ADO29564;  
XX DT 29-JUL-2004 (first entry)  
XX DE Human GPCR NPY5R, SEQ ID NO:666.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
XX transgenic mouse; neurological disorder; adrenal gland disorder;  
XX colon disorder; intestinal disorder; cardiovascular disorder;  
XX muscular disorder; blood disorder; immune disorder; bone disorder;  
XX joint disorder; metabolic disorder; nutritive disorder; cancer;  
XX kidney disorder; liver disorder; lung disorder; breast disorder;  
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;  
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
XX thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
XX cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
XX CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
XX virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
XX dermatological; antitumor; antithyroid; antiallergic; anorectic;  
XX immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
XX receptor.

XX Homo sapiens.  
XX WO2004040000-A2.  
XX 13-MAY-2004.  
XX 09-SEP-2003; 2003WO-US028226.  
XX 09-SEP-2002; 2002US-0409303P.  
XX 09-APR-2003; 2003US-0461329P.  
XX (PRIM-) PRIMAL INC.

XX Gaitanaris CA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vaesiliatis D, Zeng H;  
 XX WPI: 2004-390329/36.  
 DR N-PSDB; ADO30001.  
 XX Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX Claim 151; SEQ ID NO 666; 542pp; English.  
 PS  
 XX The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
 CC invention. Note: The full sequence data for this patent did not form part  
 CC of the printed specification; those sequences not shown were obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 455 AA;  
 Query Match 100.0%; Score 2385; DB 8; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-236; Indels 0; Gaps 0;  
 Matches 455; Conservative 0; Mismatches 0;  
 QY 1 MSFYSKQDYNMDELDYNNKTLATENNATATNSDFPVDYKSSVDDLYFLGYTF 60  
 DB 1 MSFYSKQDYNMDELDYNNKTLATENNATATNSDFPVDYKSSVDDLYFLGYTF 60  
 QY 61 VSLGLFMGNLILMALMKRKNQKTVNPLGNLAFSLVLCSPPTLSVLLDQWFG 120  
 DB 61 VSLGLFMGNLILMALMKRKNQKTVNPLGNLAFSLVLCSPPTLSVLLDQWFG 120  
 QY 121 KVMCHIMPFLOCVSVLSTLILISIAIVRYEMIKHPISSNNLTANHGYFLIATVTLGFAI 180  
 DB 121 KVMCHIMPFLOCVSVLSTLILISIAIVRYEMIKHPISSNNLTANHGYFLIATVTLGFAI 180  
 QY 181 CSPLPVHSLVELQETFSALLSRYLCVESWPDSYRIAPTISLLVQILPLVCLTVS 240  
 DB 181 CSPLPVHSLVELQETFSALLSRYLCVESWPDSYRIAPTISLLVQILPLVCLTVS 240  
 QY 241 HTSVCRSISICGLSKENRLEENEMINTLHPKSKSGPQVKLSGSHKWSYFIKHHRRYS 300  
 DB 241 HTSVCRSISICGLSKENRLEENEMINTLHPKSKSGPQVKLSGSHKWSYFIKHHRRYS 300  
 QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360

DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360  
 QY 361 RVKRSVTRIKKRSRVSFYRLTILILVPAVSMPLHLFHVVTDFNDNLISNRHFKLYVCIC 420  
 DB 361 RVKRSVTRIKKRSRVSFYRLTILILVPAVSMPLHLFHVVTDFNDNLISNRHFKLYVCIC 420  
 QY 421 HLLGMSCCCLNPILYGFNLNGIKADLVSLIHCLHM 455  
 DB 421 HLLGMSCCCLNPILYGFNLNGIKADLVSLIHCLHM 455  
 RESULT 11  
 AAE08016  
 ID AAE08016 standard; protein; 455 AA.  
 XX AC AAE08016;  
 XX 01-NOV-2001 (first entry)  
 XX African green monkey (AGM) neuropeptide Y5 (NPY5) receptor.  
 XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;  
 KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;  
 KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;  
 KW locomotor; anxiety disorder; limbic disorder; tranquilliser;  
 KW african green monkey; AGM.  
 XX Cercopithecus aethiops.  
 XX WO200155103-A2.  
 XX 02-AUG-2001.  
 XX 29-JAN-2001; 2001WO-US002804.  
 XX 28-JAN-2000; 2000US-0178652P.  
 XX (NEUR-) NEUROGEN CORP.  
 XX Bennett M, Brodbeck R, Krause J;  
 XX WPI; 2001-514543/56.  
 XX N-PSDB; AADI4746.  
 XX New chimeric receptor proteins comprising a single polypeptide chain of  
 PT amino acids, useful as targets for drug actions, and as basis for drug  
 PT discovery and development.  
 XX Example 2; Page 70-72; 72pp; English.  
 XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.  
 CC The NPY receptors are G-protein-coupled transmembrane proteins with seven  
 CC membrane spanning transmembrane (TM) domains. The compounds that modulate  
 CC the activity of a NPY receptor is useful in the preparation of a  
 CC medicament for treating conditions including obesity, high/low blood  
 CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,  
 CC seizure, locomotor and anxiety disorders. They can also be used as  
 CC targets for drug actions, and as basis for drug discovery and  
 CC development. The NPY5 receptor may have an anti-epileptic activity in the  
 CC control of limbic seizures. The present sequence is african green monkey  
 CC (AGM) NPY5 receptor  
 XX Sequence 455 AA;  
 Query Match 99.5%; Score 2373; DB 4; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 2.1e-235;  
 Matches 452; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSFYSKQDYNMDELDYNNKTLATENNATATNSDFPVDYKSSVDDLYFLGYTF 60  
 DB 1 MSFYSKQDYNMDELDYNNKTLATENNATATNSDFPVDYKSSVDDLYFLGYTF 60

QY 61 VSILGFMGNLLILMALMKKRNOKTIVNFIENLAFSDILVLPSCPTLTSVLLDQWFG 120  
 DB 61 VSILGFMGNLLILMALMKKRNOKTIVNFIENLAFSDILVLPSCPTLTSVLLDQWFG 120  
 QY 121 KVMCHIMPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGFLIATVMTLGFAL 180  
 DB 121 KVMCHIMPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGFLIATVMTLGFAL 180  
 QY 181 CSPILPVFHSVELQETFGSALLSRYLCVSWPDSYRIAFITISLLVQVILPLVCLTVS 240  
 DB 181 CSPILPVFHSVELQETFGSALLSRYLCVSWPDSYRIAFITISLLVQVILPLVCLTVS 240  
 QY 241 HTSVCRSISCGLSNKENRLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYS 300  
 DB 241 HTSVCRSISCGLSNKENRLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYS 300  
 QY 301 KKTACVLPAPEPPOENHSRILPENFGSVRSQSSSKFIPGVPTCTEIKPEENSVDYHEL 360  
 DB 301 KKTACVLPAPEPPOENHSRILPENFGSVRSQSSSKFIPGVPTCTEIKPEENSVDYHEL 360  
 QY 361 RVKRSVTRIKKRSRVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 DB 361 RVKRSVTRIKKRSRVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 QY 421 HLLGMMSCCLNPILYGLNNGIKADLVSLIHCLHM 455  
 DB 421 HLLGMMSCCLNPILYGLNNGIKADLVSLIHCLHM 455

RESULT 12

AAW27604  
 ID AAW27604 standard; protein; 445 AA.

XX AC AAW27604;  
 XX DT 14-APR-1998 (first entry)

XX DE Human neuropeptide Y receptor (NPY Y5).  
 XX KW Neurotansmitter Y receptor Y5; NPY Y5; peptide YY; NPY/YY receptor; human;  
 XX KW neurotansmitter; antagonist; agonist; obesity; anorexia;  
 XX KW hyperlipidaemia; diabetes; gene therapy; transgenic animal.

XX OS Homo sapiens.  
 XX PN WC9737998-A2.  
 XX PD 16-OCT-1997.

XX PF 08-APR-1997; 97WO-US005781.  
 XX PR 08-APR-1996; 96US-0014969P.  
 XX PA (FARB ) BAYER CORP.

XX PI Hu Y, Mccaleb ML, Bloomquist BT, Flores-Riveros JR, Cornfield LJ;  
 XX DR WPI; 1997-512637/47.  
 XX DR N-PSDB; AAT73602.

XX PT Nucleic acid molecule encoding neuro:peptide Y receptor - useful to  
 PT identify antagonists and agonists, e.g. treat obesity, diabetes,  
 PT hyperlipidaemia and anorexia.

XX PS Claim 2; Page 37-39; 49pp; English.

XX CC A novel human receptor for the neurotransmitters neuropeptide Y (NPY) and  
 CC peptide YY (PYY) is designated NPY Y5 receptor. Its amino acid sequence  
 CC was deduced from a human genomic DNA clone (see AAT87940). Rat NPY Y5 has  
 CC also been identified (see AAW27602-03). These polypeptides can be  
 CC expressed in host (e.g. human 293) cells. The effects of NPY include  
 CC blood pressure regulation, memory enhancement, anxiolysis/sedation and  
 CC increased food intake. The receptor can therefore be used to screen for

CC antagonists and agonists capable of controlling these conditions;  
 CC antagonists could be used to treat obesity and diabetes by reducing  
 CC appetite and food consumption, while agonists could be used to treat  
 CC anorexia

XX SQ Sequence 445 AA;

Query Match 97.7%; Score 2330; DB 2; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-231;  
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYKNTLATENNTAATNSDPYWDYKSSVDDLOVFLGIGLYTFVSLGFMGNL 70  
 DB 1 MDLEDEYKNTLATENNTAATNSDPYWDYKSSVDDLOVFLGIGLYTFVSLGFMGNL 50  
 QY 71 LILMALMKKRNOKTIVNFIENLAFSDILVLPSCPTLTSVLLDQWFGKVMCHIMPFL 130  
 DB 61 LILMALMKKRNOKTIVNFIENLAFSDILVLPSCPTLTSVLLDQWFGKVMCHIMPFL 120  
 QY 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGFLIATVMTLGFALCPLPVFHS 190  
 DB 121 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGFLIATVMTLGFALCPLPVFHS 180  
 QY 191 VELQETFGSALLSRYLCVSWPDSYRIAFITISLLVQVILPLVCLTVSHTSVCRSIS 250  
 DB 181 VELQETFGSALLSRYLCVSWPDSYRIAFITISLLVQVILPLVCLTVSHTSVCRSIS 240  
 QY 251 GLSNKENRLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYSKKTACVLPA 310  
 DB 241 GLSNKENRLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYSKKTACVLPA 300  
 QY 311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCTEIKPEENSVDYHELVRKSVTRIK 370  
 DB 301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCTEIKPEENSVDYHELVRKSVTRIK 360  
 QY 371 KRGRSVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLGMMSCCL 430  
 DB 361 KRGRSVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLGMMSCCL 420  
 QY 431 NPILYGLNNGIKADLVSLIHCLHM 455  
 DB 421 NPILYGLNNGIKADLVSLIHCLHM 445

RESULT 13

AAW15230  
 ID AAW15230 standard; protein; 445 AA.

XX AC AAW15230;  
 XX DT 21-JUL-1997 (first entry)

XX DE Human neuropeptide Y-Y5 receptor.  
 XX KW Neuropeptide Y-Y5; appetite; obesity; G-protein coupled receptor;  
 XX KW antiobesity; hypotensive; neuronal growth factor; cardiovascular drug;  
 XX KW anti-psychotic; neuroleptic; antidiabetic; agonist; antagonist.

XX OS Homo sapiens.  
 XX PN WO9717440-A1.

XX PD 15-MAY-1997.

XX PF 08-NOV-1996; 96WO-AU000706.  
 XX PR 09-NOV-1995; 95AU-00006467.

XX PA (GARV-) GARVAN INST MEDICAL RES.  
 XX PI Herzog H;

XX WPI; 1997-281029/25.

DR N-PSDB; AAT66909, AAT66910.  
 XX DNA encoding the neuro-peptide Y-Y5 receptor - for screening for NPY-Y5  
 PT antagonists and agonists, useful as anti-obesity agents, anti-  
 PT hypertensive agents cardiovascular drugs, etc.  
 XX  
 XX Claim 17; Fig 1; 44pp; English.  
 XX  
 XX A novel human neuropeptide Y (NPY)-Y1-like receptor (AAW15230),  
 CC designated NPY-Y5 receptor, is a G-protein coupled receptor of NPY, which  
 CC is involved in appetite/obesity regulation. Its amino acid sequence was  
 CC deduced from isolated genomic (AAT66909) and foetal brain cDNA (AAT66910)  
 CC sequences. Rat (AAW15232) and mouse (AAW15233) NPY-Y5 receptors have also  
 CC been identified. NPY-Y5 receptors can be expressed on the cell surface of  
 CC host (pref. CHO, human embryonic kidney 293 or insect Sf9) cells. The  
 CC receptors or host cells can be used to screen for NPY (ant)agonists  
 CC useful as potential hypotensives, cardiovascular drugs, neuronal growth  
 CC factors, anti-psychotic, anti-obesity or anti-diabetic drugs  
 XX  
 XX Sequence 445 AA;

Query Match 97.7%; Score 2330; DB 2; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-231;  
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYKNTLATENNTAATNSDPFVWDYKSSVDDLOQLFLGLYTFVSLGFMGNL 70  
 Db 1 MDLEDEYKNTLATENNTAATNSDPFVWDYKSSVDDLOQLFLGLYTFVSLGFMGNL 60  
 QY 71 LILMALMKRNOKTTVNFIGNLATSDILVLFCSPTLTSLVLDQWFGKVMCHIMPEL 130  
 Db 61 LILMALMKRNOKTTVNFIGNLATSDILVLFCSPTLTSLVLDQWFGKVMCHIMPEL 120  
 QY 131 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGFIATVTLGFAICSPVPVHSL 190  
 Db 121 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGFIATVTLGFAICSPVPVHSL 180  
 QY 191 VELOETFGSALLSSRYLCVESWPSDSYRTAFTISLLVQYILPLVCLTVSHTSVCRSISC 250  
 Db 181 VELOETFGSALLSSRYLCVESWPSDSYRTAFTISLLVQYILPLVCLTVSHTSVCRSISC 240  
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPQVKLSGSHKWSYFIKRRRYSKKTACVLPAP 310  
 Db 241 GLSNKENRLEENEMINLTLPKSKSGPQVKLSGSHKWSYFIKRRRYSKKTACVLPAP 300  
 QY 311 ERPSQENHSRIILPENFGSVRSOLSSSKFIQVPTCFEIKPEENSDVHELVRKSVTRIK 370  
 Db 301 ERPSQENHSRIILPENFGSVRSOLSSSKFIQVPTCFEIKPEENSDVHELVRKSVTRIK 360  
 QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGWMSCCL 430  
 Db 361 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGWMSCCL 420  
 QY 431 NPILYGLNNGIKADLVSLIHCLHM 455  
 Db 421 NPILYGLNNGIKADLVSLIHCLHM 445

RESULT 14  
 AAY14554  
 ID AAY14554 standard; protein; 445 AA.  
 XX  
 XX AAY14554;  
 XX  
 XX 31-AUG-1999 (first entry)  
 XX Human neuropeptide Y5 receptor protein.  
 XX  
 XX Human; neuropeptide Y; NPY; receptor; hypothalamus; antagonist; agonist;  
 KW obesity; diabetes; antibody; detection.  
 XX  
 XX Homo sapiens.  
 XX

PN US5919901-A.  
 XX  
 PD 06-JUL-1999.  
 XX  
 PF 08-APR-1996; 96US-00630118.  
 XX  
 PR 08-APR-1996; 96US-00630118.  
 XX  
 XX (FARB ) BAYER CORP.  
 PA  
 PI Cornfield LJ, Flores-Riveros JR, Hu Y, Mccaleb ML, Bloomquist BT;  
 XX  
 XX WPI; 1999-394648/33..  
 DR N-PSDB; AAX83197.  
 XX  
 XX Neuropeptide Y receptor Y5 and related nucleic acid.  
 PT  
 PS Claim 3; Col 29-34; 23pp; English.  
 XX

This sequence represents the human neuropeptide Y5 receptor (Y5) protein.  
 CC The protein is useful for screening for compounds able to be used as  
 CC agonists and antagonists to the Y5 receptor, especially for the treatment  
 CC obesity and diabetes and for developing antibodies for the detection of  
 CC the protein  
 XX

Query Match 97.7%; Score 2330; DB 2; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-231;  
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYKNTLATENNTAATNSDPFVWDYKSSVDDLOQLFLGLYTFVSLGFMGNL 70  
 Db 1 MDLEDEYKNTLATENNTAATNSDPFVWDYKSSVDDLOQLFLGLYTFVSLGFMGNL 60  
 QY 71 LILMALMKRNOKTTVNFIGNLATSDILVLFCSPTLTSLVLDQWFGKVMCHIMPEL 130  
 Db 61 LILMALMKRNOKTTVNFIGNLATSDILVLFCSPTLTSLVLDQWFGKVMCHIMPEL 120  
 QY 131 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGFIATVTLGFAICSPVPVHSL 190  
 Db 121 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGFIATVTLGFAICSPVPVHSL 180  
 QY 191 VELOETFGSALLSSRYLCVESWPSDSYRTAFTISLLVQYILPLVCLTVSHTSVCRSISC 250  
 Db 181 VELOETFGSALLSSRYLCVESWPSDSYRTAFTISLLVQYILPLVCLTVSHTSVCRSISC 240  
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPQVKLSGSHKWSYFIKRRRYSKKTACVLPAP 310  
 Db 241 GLSNKENRLEENEMINLTLPKSKSGPQVKLSGSHKWSYFIKRRRYSKKTACVLPAP 300  
 QY 311 ERPSQENHSRIILPENFGSVRSOLSSSKFIQVPTCFEIKPEENSDVHELVRKSVTRIK 370  
 Db 301 ERPSQENHSRIILPENFGSVRSOLSSSKFIQVPTCFEIKPEENSDVHELVRKSVTRIK 360  
 QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGWMSCCL 430  
 Db 361 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGWMSCCL 420  
 QY 431 NPILYGLNNGIKADLVSLIHCLHM 455  
 Db 421 NPILYGLNNGIKADLVSLIHCLHM 445

RESULT 15  
 AAY52578  
 ID AAY52578 standard; protein; 445 AA.  
 XX  
 XX AAY52578;  
 XX  
 XX 28-FEB-2000 (first entry)  
 XX Human NPY (neuropeptide Y) Y5 receptor.  
 DE

XX Neuropeptide Y; NPY; receptor; Y5; G-protein coupled; expression;  
KW chimeric; pharmacological property; peripheral nervous system;  
KW central nervous system; physiological; activity; food intake; feeding;  
KW thermogenesis; blood pressure; hormone release; gut motility;  
KW smooth muscle tone; sleep; circadian rhythm; neuronal excitability;  
KW nociception; mood; emotional response; seizure activity; diuresis;  
KW natriuresis; calciuresis; antinense; agonist; antagonist; obesity;  
KW hypertension; epilepsy; sexual dysfunction; jet lag.  
XX Homo sapiens.  
XX US9895616-A.  
XX 16-NOV-1999.  
XX 07-JAN-1998; 98US-00003199.  
XX 07-JAN-1998; 98US-00003199.  
XX (SCHE ) SCHERING CORP.  
XX Parker EM, Rudinski MS, Strader CD;  
XX WPI; 2000-012792/01.  
XX N-PSDB; AAZ46232.  
XX Chimeric mammalian neuropeptide Y5 receptor polypeptides useful for  
PT treating a range of disorders including jet lag, hypertension and sexual  
XX dysfunction.  
XX Example; Col 37-40; 24pp; English.  
XX This sequence represents human neuropeptide Y (NPY) Y5 receptor, cDNA  
CC encoding which was isolated and amplified from a human neuroblastoma cell  
CC line using primers AAZ46215-246223. The receptor was transiently  
CC expressed in COS1 cells, but its level of expression was found to be  
CC significantly lower in comparison to that of the rat NPY Y5 receptor  
CC (AAV52579). The invention relates to a chimeric rat/human NPY receptor,  
CC comprising the 5' untranslated region (5' UTR) and extreme 5' coding  
CC region (105 bp) of the rat Y5 receptor cDNA, appended to nucleotides 365-  
CC 1633 of the human Y5 receptor cDNA. When transfected into COS1 cells, the  
CC chimeric construct yielded levels of expression higher than the native  
CC human Y5 receptor, and similar or greater levels of expression than the  
CC native rat Y5 receptor. The pharmacological properties of the chimeric  
CC receptor were similar to those of the native human Y5 receptor. NPY is  
CC widely distributed in both the peripheral and central nervous systems and  
CC has a wide range of physiological activities including effects on food  
CC intake, thermogenesis, blood pressure, hormone release, gut motility,  
CC smooth muscle tone, sleep and circadian rhythms, neuronal excitability,  
CC nociception, mood and emotional responses. NPY mediates these  
CC physiological effects via interactions with at least six distinct G-  
CC protein coupled receptors (designated Y1-Y6). The Y5 receptor mediates  
CC the effects of NPY on feeding, thermogenesis, neuronal excitability and  
CC seizure activity, diuresis, natriuresis and calciuresis. The chimeric Y5  
CC receptor, associated nucleic acids (e.g., expression vectors or antisense  
CC molecules), agonists or antagonists may be administered to treat  
CC disorders such as obesity, hypertension, epilepsy, sexual dysfunction and  
CC jet lag associated with abnormal expression/activity of NPY  
XX  
XX Sequence 445 AA;  
SQ

Query Match 97.7%; Score 2330; DB 3; Length 445;  
Best Local Similarity 100.0%; Pred. No. 5.5e-231;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYNNKTLATENNATARNSDFFPWDDYKSSVDDQYFLIGLYTFVSLGFMGNL 70  
DB 1 MDLEDEYNNKTLATENNATARNSDFFPWDDYKSSVDDQYFLIGLYTFVSLGFMGNL 60  
QY 71 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFMGKVMCHIMPFL 130  
DB 61 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFMGKVMCHIMPFL 120

QY 131 QCVSVLSTLILISIAIVRHKIPISNNLTANHGFLIATVMTGLFAICSPLPVFHSL 190  
DB 121 QCVSVLSTLILISIAIVRHKIPISNNLTANHGFLIATVMTGLFAICSPLPVFHSL 180  
QY 191 VELOETFGSALLSRYLCVSWPDSYRIARTISLLVQVYILPLVCLTVSHTSVCRSTSC 250  
DB 181 VELOETFGSALLSRYLCVSWPDSYRIARTISLLVQVYILPLVCLTVSHTSVCRSTSC 240  
QY 251 GLSNKENLEENEMINLTLPSSKSGPOVKLSGSHKMSYSPFKHRRYSKKTACVLPAP 310  
DB 241 GLSNKENLEENEMINLTLPSSKSGPOVKLSGSHKMSYSPFKHRRYSKKTACVLPAP 300  
QY 311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCTEIKPEENSVDVHELVRKSVTEIK 370  
DB 301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCTEIKPEENSVDVHELVRKSVTEIK 360  
QY 371 KRSRSVFYRLTILVFAVSWMPHLPHVWTFDNDNLISNRHFKLVYICIHLLGWMSCCL 430  
DB 361 KRSRSVFYRLTILVFAVSWMPHLPHVWTFDNDNLISNRHFKLVYICIHLLGWMSCCL 420  
QY 431 NPILYGFLLNGIKADLVSLIHCLHM 455  
DB 421 NPILYGFLLNGIKADLVSLIHCLHM 445

Search completed: October 21, 2004, 12:09:59  
Job time : 156 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 21, 2004, 11:59:55 ; Search time 40 Seconds  
(without alignments)  
1094.456 Million cell updates/sec

Title: US-09-771-956-13

Perfect score: 2385

Sequence: 1 NSFYKQDYNMDELDEYNN.....GFLNNGIKADLVSLHCLHM 455

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Match | Length | DB ID    | Description        |
|------------|-------|-------|--------|----------|--------------------|
| 1          | 481.5 | 20.2  | 366    | 2 S71152 | neuropeptide Y/pep |
| 2          | 481.5 | 20.2  | 384    | 2 A45490 | neuropeptide Y/pep |
| 3          | 480   | 20.1  | 349    | 2 S12863 | G protein-coupled  |
| 4          | 480   | 20.1  | 382    | 2 B41333 | neuropeptide Y/pep |
| 5          | 480   | 20.1  | 382    | 2 S27388 | neuropeptide Y/pep |
| 6          | 464.5 | 19.5  | 375    | 2 I32182 | neuropeptide Y/pep |
| 7          | 463.5 | 19.4  | 375    | 2 G02300 | pancreatic polypep |
| 8          | 458   | 19.2  | 375    | 2 S63685 | neuropeptide Y/pep |
| 9          | 455.5 | 19.1  | 381    | 2 I39187 | neuropeptide Y/pep |
| 10         | 404   | 16.9  | 370    | 1 I52315 | G protein-coupled  |
| 11         | 384   | 16.1  | 584    | 2 JC7809 | sulfakinin recepto |
| 12         | 377   | 15.8  | 436    | 2 JC5599 | cholecystokinin-A  |
| 13         | 375   | 15.7  | 427    | 2 S05150 | gastric CCK-A rece |
| 14         | 368.5 | 15.5  | 444    | 2 A42685 | cholecystokinin re |
| 15         | 367   | 15.4  | 449    | 2 A41738 | neuropeptide Y/pep |
| 16         | 356   | 14.9  | 428    | 2 JN0692 | cholecystokinin ty |
| 17         | 355.5 | 14.9  | 430    | 2 I51898 | cholecystokinin A  |
| 18         | 351.5 | 14.7  | 447    | 2 A47430 | gastrin/cholecysto |
| 19         | 347   | 14.5  | 455    | 2 T15622 | hypothetical prote |
| 20         | 343.5 | 14.4  | 453    | 2 S32817 | gastrin receptor - |
| 21         | 339.5 | 14.2  | 452    | 2 JC2459 | gastrin/cholecysto |
| 22         | 329.5 | 13.8  | 450    | 2 JQ1614 | gastrin receptor - |
| 23         | 329.5 | 13.8  | 452    | 2 A46195 | cholecystokinin B  |
| 24         | 320   | 13.4  | 423    | 2 B40470 | glucocorticoid-ind |
| 25         | 316.5 | 13.3  | 457    | 2 T29741 | hypothetical prote |
| 26         | 309.5 | 13.0  | 423    | 2 JC7677 | allatostatin recep |
| 27         | 308.5 | 12.9  | 394    | 2 JC7209 | gastrin receptor - |
| 28         | 306.5 | 12.9  | 365    | 2 T20184 | hypothetical prote |
| 29         | 303   | 12.7  | 399    | 2 T16277 | hypothetical prote |

## RESULT 1

S71152

neuropeptide Y/peptide YY receptor Y1 - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 27-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S71152; S55924

R;Martens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.

submitted to the EMBL Data Library, November 1993

A;Description: Cloning and sequencing of an neuropeptide Y/peptide YY receptor from Xenop

A;Reference number: S71152

A;Accession: S71152

A;Molecule type: mRNA

A;Residues: 1-366 <NAR>

A;Cross-references: UNIPROT:P34992; EMBL:L25416; NID:G409169; PIDN:AAA49918.1; PID:G4091

R;Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.

Biochim. Biophys. Acta 1261, 439-441, 1995

A;Title: Cloning and sequence analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA fr

A;Reference number: S55924; MUID:95260870; PMID:7742373

A;Accession: S55924

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-278, 'T', 280-366 <BLO>

A;Cross-references: EMBL:L25416; NID:G409169

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 20.2%; Score 481.5; DB 2; Length 366;

Best Local Similarity 26.4%; Pred. No. 6e-31;

Matches 114; Conservative 75; Mismatches 128; Indels 115; Gaps 8;

|    |     |  |
|----|-----|--|
| QY | 19  | YNKTLATENTATATNSDPFVWDYKSSVDDQLQVFLGL-YTFVSLGFGMGNLLILMALM 77  |
| Db | 6   | YFENISVPNNISG--NITFFISEDALPLP--MFTLALAYCAVILGLSGLNLIIL 61      |
| QY | 78  | KRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQWFGKVMCHIMPFCQSVLV 137       |
| Db | 62  | KQKERNVTNIIIVNLSFSDLIATMCLPFTLIYTLMDHWFGEVMCKLNEYIQCVSVTV 121  |
| QY | 138 | STLILISIAIVRYHMKHPISNNLTANHYFLIATVTLGFAICSLPVPVHSLVELOTF 197   |
| Db | 122 | SIFSVLIAIEHQILINPRGRPNRHACGIVINGFAMACSTPLMVMYSVLTD--EPP 179    |
| QY | 198 | GSALLSS---RYLCVESWPSDSYRIAFITISLLVQYLPLVCLTVSHTSVCRISCSLSN 254 |
| Db | 180 | KNISLDSVIGKYVCLEDFDKFRISYTTLLFIQLQGLFCIFVCYTKI----- 229        |
| QY | 255 | KENRLEENEMINLTLPKSGQPKVLSGSHKWSYFIKKHRRYSKKTACVLPAPERPS 314    |
| Db | 230 | -----FRLKRR----- 236   |
| QY | 315 | QENHGRILLPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSVDVHLEKSVTRIKRKR 374 |

neurokinin 2 recep  
hypothetical prote  
glucocorticoid-ind  
hypothetical prote  
galanin receptor 1  
protein AC7.1 [imp  
hypothetical prote  
probable allatosta  
gastrin-releasing  
neurokinin 2 recep  
tachykinin recepto  
dopamine receptor-  
neurokinin 2 recep  
neurokinin 3 recep  
neurokinin 3 recep

## ALIGNMENTS

```

Db      237 -----NNMDKLRDNKYRSSETKR-- 255
QY      375 SVFYRLTILILVFAVSMPLHLPHVVDNDNLISNRHFKLVYICHLGMMSCCLNPIL 434
Db      256 -INIMLLSVGWGFAFLFFIFNLVFDWNHEAVATCNHLLFLICHLTAMISTCWNPIF 314
QY      435 YGFLNNGIKADL 446
Db      315 YGFLNKNFORDL 326

RESULT 2
A:Species: Homo sapiens (man)
A:Title: neurotrophin Y receptor Y1 - human
A:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A:Accession: A45490; A46133; A42773
R:Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
J. Biol. Chem. 268, 6703-6707, 1993
A:Title: Genomic organization, localization, and allelic differences in the gene for the
A:Reference number: A45490; MUID:93203272; PMID:8095935
A:Accession: A45490
A:Molecule type: DNA
A:Residues: 1-384 <HER>
A:Cross-references: UNIPROT:P25929; GI:L07615; NID:G189284; PIDN:AAA59947.1; PID:G189285
A:Note: sequence extracted from NCBI backbone (NCBIN:128005, NCBI:P:128000)
R:Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A:Title: Cloned human neurotrophin Y receptor couples to two different second messenger
A:Reference number: A46133; MUID:92335184; PMID:1321422
A:Accession: A46133
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-384 <HE2>
A:Note: sequence extracted from NCBI backbone (NCBI:P:108538)
R:Larhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlsted, C.
J. Biol. Chem. 267, 10938-10939, 1992
A:Title: Cloning and functional expression of a human neurotrophin Y peptide YY receptor
A:Reference number: A42773; MUID:92283782; PMID:1317848
A:Accession: A42773
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-384 <LAE>
A:Cross-references: GI:M88461; NID:G189155; PIDN:AAA73215.1; PID:G189156
A:Experimental source: fetal brain
A:Note: sequence extracted from NCBI backbone (NCBIN:104735, NCBI:P:104736)
C:Genetics:
A:Gene: GDB:NPY1R; NPYR
A:Cross-references: GDB:132643; OMIM:162641
A:Map position: 4q31.3-4q32
C:Superfamily: neurokinin 1 receptor
C:Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
F:37-66/Domain: transmembrane #status predicted <TM1>
F:77-103/Domain: transmembrane #status predicted <TM2>
F:118-136/Domain: transmembrane #status predicted <TM3>
F:155-179/Domain: transmembrane #status predicted <TM4>
F:209-232/Domain: transmembrane #status predicted <TM5>
F:261-286/Domain: transmembrane #status predicted <TM6>
F:300-323/Domain: transmembrane #status predicted <TM7>
F:113-198/Disulfide bonds: #status predicted
F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:338/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match      20.2%; Score 481.5; DB 2; Length 384;
Best Local Similarity 26.3%; Pred. No. 6.4e-31;
Matches 115; Conservative 76; Mismatches 129; Indels 117; Gaps 8;

QY      20 NKTLL--ATENNNTA----ATRNDFPVDYDKSSVDDQLQYFLIGL-YTFVSLGFMGNLLI 72
Db      2 NSTLFSQVNHSHVSNFSEKNAQLAFENDDCHLPLAMIFTLALAYGAVILGVSGNLAL 61
QY      73 LMALMKRNQKTTNVLNGLAFSDILVLFCSFPTLTSVLLDQWFGKVNCHIMPFLQ 132

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Db      62 IIIILKOKERNVTNLIIVNLSFSDLLVAIMCLPFTFYVTLMDHWVFGEMACKLNPFVQC 121
QY      133 VSLVSTLIILISAIYRYHMKHPIFNLTANHYGLIATVTLGFAICSPLPVHFSLVE 192
Db      122 VSTISVFSVLVIAVERHQLIINPRGWRPNRHAYGVIAVWL--AVASSLPFLYQVM 179
QY      193 LQETFGSALLSS--RYLCVESWPSYSYIAFTISILLVQYILPLVCLTVSHTSVCRSIS 249
Db      180 TDEPFQNVTLDAYDKYVCFDQFSDSHRLSYTLTLLVLYQYFGFLCFIFICYFKI---- 234
QY      250 CGLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYRYSKKTACVLPA 309
Db      235 -----YRLKRR----- 241
QY      310 PERPSQENHRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDVHELVRKSVTRI 369
Db      242 -----NNMDKMRDNKYRSSE 257
QY      370 KESRSVYFRLTILILVEAVSMPLHLPHVVDNDNLISNRHFKLVYICHLGMMSCC 429
Db      258 TKR---INIMLLSVVAPVAVCMPLTIFNTVFDWNHQLIATCNHLLFLICHLTAMISTC 314
QY      430 LNPILYGLNNGIKADL 446
Db      315 VNPIFYGLNKNFORDL 331

RESULT 3
S12863
G protein-coupled receptor FCS - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: S12863; S19101
R:Eva, C.; Keinenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.
FEBS Lett. 271, 81-84, 1990
A:Title: Molecular cloning of a novel G protein-coupled receptor that may belong to the
A:Reference number: S12863; MUID:91032093; PMID:2172008
A:Accession: S12863
A:Molecule type: mRNA
A:Residues: 1-349 <EVA>
A:Cross-references: UNIPROT:P21555; EMBL:Z11504
R:Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.
submitted to the EMBL Data Library, November 1991
A:Description: Pharmacological and Transduction Properties of a Recombinantly Expressed
A:Reference number: S19101
A:Accession: S19101
A:Molecule type: mRNA
A:Residues: 1-343; DDYETIAMSTMTDVSSTLSKQASPVAFKISVNDNEKI' <KRA>
A:Cross-references: EMBL:Z11504; NID:G57636; PIDN:CAA77579.1; PID:G57637
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F:73-93/Domain: transmembrane #status predicted <TM1>
F:114-135/Domain: transmembrane #status predicted <TM2>
F:155-175/Domain: transmembrane #status predicted <TM3>
F:213-233/Domain: transmembrane #status predicted <TM4>
F:262-285/Domain: transmembrane #status predicted <TM5>
F:299-322/Domain: transmembrane #status predicted <TM6>
F:2,11,17/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:346/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match      20.1%; Score 480; DB 2; Length 349;
Best Local Similarity 25.9%; Pred. No. 7.5e-31;
Matches 114; Conservative 74; Mismatches 127; Indels 126; Gaps 9;

QY      20 NKTLL--ATENNNTA----ATRNDFPVDYDKSSVDDQLQYFLIGLYTF-----VSLGFMG 68
Db      2 NSTLFSRVNYSVHVNSNSPFLAFEN----DCHLPLAVIFTLALAYGAVILGVSG 56
QY      69 NLLIILMALMKRNQKTTNVLNGLAFSDILVLFCSFPTLTSVLLDQWFGKVNCHIMP 128
Db      57 NLLIILKOKERNVTNLIIVNLSFSDLLVAVMCLPFTFYVTLMDHWVFGEMACKLN 116

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QY 129 FLOCVSVLSTLLISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGFALCSPLPVFH 188  
 Db 117 FVQCVSITVSIFSLVIAVERHQLIINPGWPNRHHAYIGITVIAVLAVASSLPFVIYQ 176  
 QY 189 SLVELOETFGSALLSS---RYLCVESWPSDSYRIAFITSLLLVQYILPLVCLTVSHTSVC 245  
 Db 177 ILTD--EPFQNVSLAAFKDKYVCFDPKPSDSHRLSYTTLLLVQYFGPLCFIFICYFKI- 233  
 QY 246 RSISCGLSNKENLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYSKKTAC 305  
 Db 234 ---YIRLKRNNMMDK----- 246  
 QY 306 VLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHELVRKRS 365  
 Db 247 ---IRDSKYRSSE----- 256  
 QY 366 VTRIKKRSRVFRLTILILFAVSWMPHLPHVVTDFNDNLISNRHFKLVYICHLGGM 425  
 Db 257 ---TKRINMLLSIVVAFVAVCWMLPTITFNTVFDWNNHQIATCNHNLFLCHLTAM 309  
 QY 426 MSCCLNPILYGFNLNGIKADL 446  
 Db 310 ISTCVNPIFYGFNLKNFORDL 330

## RESULT 4

B46133

neuropeptide Y/peptide YY receptor Y1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Apr-2000

C;Accession: B46133

R;Herzog, H.; Host, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992

A;Title: Cloned human neuropeptide Y receptor couples to two different second messenger

A;Reference number: A46133; MUID:92335184; PMID:1321422

A;Accession: B46133

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-382 &lt;HER&gt;

A;Note: sequence extracted from NCBI backbone (NCBIP:108539)

C;Superfamily: neurokinin 1 receptor

C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 20.1%; Score 480; DB 2; Length 382;  
 Best Local Similarity 25.9%; Pred. No. 8.4e-31;  
 Matches 114; Conservative 74; Mismatches 127; Indels 126; Gaps 9;

QY 20 NKTLL--ATENNTA---ATNSDPVWDYKSSVDDLYQLYFLIGLYTF-----VSLDGMG 68  
 Db 2 NSTLFRVENYSHYVNSNSPLAPEN-----DCHLPLAVIPLTALAYGAVILGVSG 56  
 QY 69 NLAILMALMKRNQKTTNVLNLAFLSDILVLFCSPTLTSVLLDQWMEGKVMCHIMP 128  
 Db 57 NLALIIILKQEMRNVTNLIWNLSFSDLLVAVMCLPPTFVYTLMDHWFGETMCKLNP 116  
 QY 129 FLOCVSVLSTLLISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGFALCSPLPVFH 188  
 Db 117 FVQCVSITVSIFSLVIAVERHQLIINPGWPNRHHAYIGITVIAVLAVASSLPFVIYQ 176  
 QY 189 SLVELOETFGSALLSS---RYLCVESWPSDSYRIAFITSLLLVQYILPLVCLTVSHTSVC 245  
 Db 177 ILTD--EPFQNVSLAAFKDKYVCFDPKPSDSHRLSYTTLLLVQYFGPLCFIFICYFKI- 233  
 QY 246 RSISCGLSNKENLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYSKKTAC 305  
 Db 234 ---YIRLKRNNMMDK----- 246  
 QY 306 VLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHELVRKRS 365  
 Db 247 ---IRDSKYRSSE----- 256  
 QY 366 VTRIKKRSRVFRLTILILFAVSWMPHLPHVVTDFNDNLISNRHFKLVYICHLGGM 425

Db 257 ---TKRINMLLSIVVAFVAVCWMLPTITFNTVFDWNNHQIATCNHNLFLCHLTAM 309  
 QY 426 MSCCLNPILYGFNLNGIKADL 446  
 Db 310 ISTCVNPIFYGFNLKNFORDL 330

RESULT 5  
 S27388  
 neuropeptide Y receptor NPY-1 - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S27388  
 R;Eva, C.; Oberto, A.; Sprengel, R.; Genazzani, R.  
 FEBS Lett. 314, 285-288, 1992  
 A;Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific ex  
 A;Reference number: S27388; MUID:93106169; PMID:1468559  
 A;Accession: S27388  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-382 <EVA>  
 A;Cross-references: UNIPROT:Q04573; EMBL:Z18280; NID:g53438; PIDN:CAA79157.1; PID:g53439  
 C;Superfamily: neurokinin 1 receptor

Query Match 20.1%; Score 480; DB 2; Length 382;  
 Best Local Similarity 25.9%; Pred. No. 8.4e-31;  
 Matches 114; Conservative 75; Mismatches 126; Indels 126; Gaps 9;

QY 20 NKTLL--ATENNTA---ATNSDPVWDYKSSVDDLYQLYFLIGLYTF-----VSLDGMG 68  
 Db 2 NSTLFSKVENSHYVNSNSPLAPEN-----DCHLPLAVIPLTALAYGAVILGVSG 56  
 QY 69 NLAILMALMKRNQKTTNVLNLAFLSDILVLFCSPTLTSVLLDQWMEGKVMCHIMP 128  
 Db 57 NLALIIILKQEMRNVTNLIWNLSFSDLLVAVMCLPPTFVYTLMDHWFGETMCKLNP 116  
 QY 129 FLOCVSVLSTLLISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGFALCSPLPVFH 188  
 Db 117 FVQCVSITVSIFSLVIAVERHQLIINPGWPNRHHAYIGITVIAVLAVASSLPFVIYQ 176  
 QY 189 SLVELOETFGSALLSS---RYLCVESWPSDSYRIAFITSLLLVQYILPLVCLTVSHTSVC 245  
 Db 177 ILTD--EPFQNVSLAAFKDKYVCFDPKPSDSHRLSYTTLLLVQYFGPLCFIFICYFKI- 233  
 QY 246 RSISCGLSNKENLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYSKKTAC 305  
 Db 234 ---YIRLKRNNMMDK----- 246  
 QY 306 VLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHELVRKRS 365  
 Db 247 ---IRDSKYRSSE----- 256  
 QY 366 VTRIKKRSRVFRLTILILFAVSWMPHLPHVVTDFNDNLISNRHFKLVYICHLGGM 425  
 Db 257 ---TKRINMLLSIVVAFVAVCWMLPTITFNTVFDWNNHQIATCNHNLFLCHLTAM 309  
 QY 426 MSCCLNPILYGFNLNGIKADL 446  
 Db 310 ISTCVNPIFYGFNLKNFORDL 330

## RESULT 6

I39182

neuropeptide Y/peptide YY receptor Y4 - human

C;Species: Homo sapiens (man)

C;Date: 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C;Accession: I39182

R;Bard, J.A.; Walker, M.W.; Branchek, T.A.; Weinshank, R.L.

J. Biol. Chem. 270, 26762-26765, 1995

A;Title: Cloning and functional expression of a human Y4 subtype receptor for pancreatic

A;Reference number: I39182; MUID:96070761; PMID:7592911

A;Accession: I39182







Db 252 ERKASTGSGFEDNDGCLQR-SKPTQLEQLQOLSGGGRRVSRHSS----- 298  
QY 349 IKEEENSVDHLEKRSVTRIKRSRSVYRITLILVAVSWPLHUFHVVTDFNNDLI 408  
Db 299 -----SSAALMAKRRVIRM-----LNVIVLFFLCWMPFISANAWRAYDTVSA 342  
QY 409 SNRHPKLVYICHLGMMSCCLNIPLYGFLNNGIKADLVSLIHC 452  
Db 343 ERLSGTPTSFILLSYTSVCNPIIYCPMKRFLGFWATPPC 386

RESULT 14  
A42685  
Cholecystokinin receptor type A - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A42685; J04225; F02213  
R;Wank, S.A.; Watkins, R.; Jensen, R.T.; Shapira, H.; de Weerth, A.; Slattey, T.  
Proc. Natl. Acad. Sci. U.S.A. 89, 3125-3129, 1992  
A;Title: Purification, molecular cloning, and functional expression of the cholecystokinin  
A;Reference number: A42685; MUID:92212981; PMID:1313582  
A;Accession: A42685  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-444 <MAN>  
A;Cross-references: UNIPROT:P30551; GB:M88096; NID:9203383; PIDN:AAA40899.1; PID:G203384  
A;Experimental source: pancreas  
A;Note: Sequence extracted from NCBI backbone (NCBI:93814, NCBI:P:93815)  
R;Takata, Y.; Takiguchi, S.; Funakoshi, A.; Kono, A.  
Biochem. Biophys. Res. Commun. 213, 958-966, 1995  
A;Title: Gene structure of rat cholecystokinin type-A receptor.  
A;Reference number: J04225; MUID:95382845; PMID:7654260  
A;Accession: J04225  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-223 <TAK>  
A;Cross-references: DDBJ:D50608; NID:G1100752  
R;Mantamadiotis, T.; Baldwin, G.S.  
Biochem. Biophys. Res. Commun. 201, 1382-1389, 1994  
A;Title: The seventh transmembrane domain of gastrin/CKK receptors contributes to non-pe  
A;Reference number: PC2213; MUID:94296413; PMID:8024583  
A;Accession: PC2213  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 366-389 <MAN>  
C;Comment: This G-protein-coupled receptor is present in the gastrointestinal system, va  
ducing the subsequent release of intracellular calcium.  
C;Genetics:  
A;Gene: CCKAR  
A;Introns: 53/1; 137/1; 224/2; 267/1  
C;Superfamily: neurokinin 1 receptor  
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein  
F;57-82/Domain: transmembrane #status predicted <TM1>  
F;93-119/Domain: transmembrane #status predicted <TM2>  
F;131-151/Domain: transmembrane #status predicted <TM3>  
F;173-193/Domain: transmembrane #status predicted <TM4>  
F;225-249/Domain: transmembrane #status predicted <TM5>  
F;330-348/Domain: transmembrane #status predicted <TM6>  
F;366-389/Domain: transmembrane #status predicted <TM7>

Query Match 15.5%; Score 368.5; DB 2; Length 444;  
Best Local Similarity 24.3%; Pred. No. 8.5e-22;  
Matches 106; Conservative 86; Mismatches 17; Indels 73; Gaps 12;

QY 23 LATENTATRNDFPVDWDDYKSSVDDLOQYFLIGLYTFTVSLGFGNLLIIMALKRKNQ 82  
Db 35 LGLENETFLCLOQPS-KEWOSALQIL-----LYSIFLLSVLGNLTIVTLIRNKR 87  
QY 83 KITWPLIGNAFSDILVFLFCSPFTLTSVLLDQWFGKWMCHIMPFCQCVSLVSLTIL 142  
Db 88 RTVTNIFLSLAVSDMLCLFCWPNLNLKDFISAVCKITFTWGTSVSVTFNL 147

QY 143 ISIAIVRHMKHPISNNL--TANHGYPILATVTLGFAICSPPLVPVSHSLVLOETFGSA 200  
Db 148 VAISLEERGAICRPQSRVQWTKSHALKVIAATCLSTIMTPYIYENLVFFTKNNQT 207  
QY 201 LLSSRYLCVESWPSDSYRIATISILLVQYILPLVCLTVSHTSVCRSISCOLSKNENLE 260  
Db 208 ANMCRFL-----PSDAMQSQWTFLLILFLPGIVMVVAYGLISLELYQGIKFDASQ-- 261  
QY 261 ENEMINLTLHPSKSKSQPVKLS-QSHKWSYSFIKHHRRYSKKTACVLPAPERFSQENHS 319  
Db 262 -----KSAKCKPSTGS-----STRYEDSDGCVLQKSRPRLKLEQ 298  
QY 320 RILPENFGSVRSQSSSSSKFPGVPTCEIKPEENSVDHLEVRKSVTRIKKRSRVFYR 379  
Db 299 QLSSGGSGSLNRIRSS-----SSAANLIARVRM----- 330  
QY 380 LILILLVAVSWPLHUFHVVTDFNNDLISNRHFK--LVYICHLGMMSCCLNIPLYG 436  
Db 331 LIVIVLFFLCWMPFISANAWRAY-DTVAEKHLSGTPIFIL--LLSYTSSCVNPIYC 387  
QY 437 FLNNGIKADLVSLIHC 452  
Db 388 FMKRRFLGFWATPPC 403

RESULT 15  
A41738  
neuropeptide Y receptor - fruit fly (Drosophila melanogaster)  
N;Alternate names: G protein-coupled receptor PR4  
C;Species: Drosophila melanogaster  
C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: A41738  
R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.  
J. Biol. Chem. 267, 9-12, 1992  
A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide 1  
A;Reference number: A41738; MUID:92112730; PMID:1370455  
A;Accession: A41738  
A;Molecule type: mRNA  
A;Residues: 1-449 <LIA>  
A;Cross-references: UNIPROT:P25931; GB:M81490; NID:G157996; PIDN:AAA28727.1; PID:G157997  
C;Genetics:  
A;Gene: FlyBase:NepYr  
A;Cross-references: FlyBase:FBgn0004842  
C;Superfamily: neurokinin 1 receptor  
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 15.4%; Score 367; DB 2; Length 449;  
Best Local Similarity 22.8%; Pred. No. 1.1e-21;  
Matches 99; Conservative 66; Mismatches 123; Indels 146; Gaps 12;

QY 41 DDYKSSVDDL---QYFLI---GLYTFVSLGFGNLLIIMALKRKNQKTTVNLIGNLA 94  
Db 74 DDYDLSDDMMSSAYFKIIVMLYIPIFALIGNTCVIVYVSTPRMRTVNYFIASLA 133  
QY 95 FSDILVFLFCSPFTLTSV-LLDQWFGKWMCHIMPFCQCVSLVSLTILISIAIVRVHMI 153  
Db 134 IGDILMSFCESSPISFILNYWFFGLALCHFNYSQAVSLVSVATYVAISIDRIVAI 193  
QY 154 KHPISNNLTANHGYPILATVTLGFAICSPPLV-----FHSVLVEQETFGSALLS 203  
Db 194 MWPLPRITKRYATFIAGVWFIALATALPIPIVSGLDIPMSPHTKCE----- 242  
QY 204 SYLQCVSWPSDSYRIATISILLVQYILPLVCLTVSHTSVCRSISCOLSKNENLENE 263  
Db 243 -KYICREWPSRSQBYTYTLLSFALQVPLGVILFYARITRV----- 286  
QY 264 MINLTLHPSKSKSGPOVKLSGSHKWSYSFIKHHRRYSKKTACVLPAPERFSQENHSRILP 323  
Db 287 -----WA-----KRP----- 291  
QY 324 ENFGSVRSQSSSKFIPGVPTCEIKPEENSVDHLEVRKSVTRIKKRSRVFYRLTIL 383

```

Db      292 -----PG-----EATNRDQRMARSKRKKVKM-----MLTV 317
QY      384 ILVFAVSWPLHLFHVVTDFNDNLISNRHF-----KLVYICICHLGMMSCCLNPILYGF 437
Db      318 VIVFTCCWLPFNILQL-----LNDEEFHWDPLPYVWFAPFWLASHCCYNPIIYCY 370
QY      438 LNNGIKADLVSLIH 451
Db      371 MNARFRSGFVQLMH 384

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Search completed: October 21, 2004, 12:14:03  
 Job time : 42 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 11:57:55 ; Search time 192 Seconds  
(without alignments)  
1363.518 Million call updates/sec

Title: US-09-771-956-13

Perfect score: 2385  
Sequence: 1 MGFYSQDYNDLDEYNN.....GFLNNGIKADLVSLHCLHM 455

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 2385  | 100.0       | 455    | 1     | Q15761 homo sapien |
| 2          | 2330  | 97.7        | 445    | 2     | Aah42416           |
| 3          | 2318  | 97.2        | 445    | 2     | Q9GK73 macaca mula |
| 4          | 2241  | 94.0        | 446    | 2     | Q925f1 cavia porce |
| 5          | 2227  | 93.4        | 446    | 1     | Q63729 canis famil |
| 6          | 2084  | 87.4        | 456    | 1     | Q63634 rattus norv |
| 7          | 2070  | 86.8        | 466    | 1     | O70342 mus musculu |
| 8          | 2070  | 86.8        | 466    | 2     | Bac32426 mus muscu |
| 9          | 2028  | 85.0        | 446    | 1     | Q97969 sus scrofa  |
| 10         | 1629  | 58.3        | 443    | 2     | Q8QFM2 gallus gall |
| 11         | 558   | 23.4        | 377    | 2     | O73733             |
| 12         | 527   | 22.1        | 348    | 2     | Q6Y6A4             |
| 13         | 527   | 22.1        | 348    | 2     | AA062565           |
| 14         | 522   | 21.9        | 373    | 2     | Q6Y6A5             |
| 15         | 522   | 21.9        | 373    | 2     | AA062564           |
| 16         | 502   | 21.1        | 377    | 2     | Q8QSM3             |
| 17         | 497   | 20.8        | 371    | 1     | Q6Y6A4             |
| 18         | 487   | 20.4        | 382    | 1     | Q6Y6A5             |
| 19         | 487   | 20.4        | 383    | 1     | Q6Y6A4             |
| 20         | 484   | 20.3        | 395    | 2     | Q8QFM1             |
| 21         | 481   | 20.2        | 366    | 1     | Q6Y6A5             |
| 22         | 481   | 20.2        | 366    | 1     | Q6Y6A4             |
| 23         | 481   | 20.2        | 384    | 1     | Q6Y6A5             |
| 24         | 481   | 20.2        | 384    | 2     | AA062564           |
| 25         | 481   | 20.2        | 384    | 2     | AA062565           |
| 26         | 481   | 20.2        | 383    | 1     | Q6Y6A4             |
| 27         | 480   | 20.1        | 382    | 1     | Q6Y6A5             |
| 28         | 480   | 20.1        | 382    | 1     | Q6Y6A4             |
| 29         | 480   | 20.1        | 382    | 2     | AA062564           |
| 30         | 476   | 20.0        | 371    | 1     | Q6Y6A5             |
| 31         | 476   | 20.0        | 371    | 2     | Bac26875           |

|    |       |      |     |   |            |            |             |
|----|-------|------|-----|---|------------|------------|-------------|
| 32 | 473.5 | 19.9 | 385 | 1 | NY2R_CHICK | Q9cdn6     | gallus gall |
| 33 | 471   | 19.7 | 374 | 2 | Q9YHX1     | Q9yhx1     | gadus morhu |
| 34 | 466   | 19.5 | 375 | 2 | Q9Y505     | sus scrofa | Q97505      |
| 35 | 464.5 | 19.5 | 375 | 1 | NY4R_HUMAN | P50391     | homo sapien |
| 36 | 464.5 | 19.5 | 375 | 2 | Q6PH06     | Q6fho6     | homo sapien |
| 37 | 464   | 19.5 | 375 | 1 | NY4R_RAT   | Q63447     | rattus norv |
| 38 | 463.5 | 19.4 | 375 | 2 | O57463     | O57463     | brachydanio |
| 39 | 462   | 19.4 | 375 | 2 | Q6YHV0     | Q6yhv0     | macaca mula |
| 40 | 462   | 19.4 | 375 | 2 | AA028939   | AA028939   | macaca mula |
| 41 | 459   | 19.2 | 371 | 2 | Q5Y6A6     | Q5y6de     | squalus aca |
| 42 | 459   | 19.2 | 371 | 2 | AA062563   | AA062563   | squalus aca |
| 43 | 458.5 | 19.2 | 381 | 2 | Q8BWW1     | Q8bww1     | mus musculu |
| 44 | 458.5 | 19.2 | 385 | 1 | NY2R_MOUSE | P97295     | mus musculu |
| 45 | 458   | 19.2 | 375 | 1 | NY4R_MOUSE | Q61041     | mus musculu |

## ALIGNMENTS

### RESULT 1

|            |  |                 |         |
|------------|--|-----------------|---------|
| NY2R_HUMAN | STANDARD;  | PRT;            | 455 AA. |
| ID         | NY5R_HUMAN   | Q15761; Q92916; |         |
| AC         | Q15761; Q92916;  |                 |         |
| DT         | 01-NOV-1997 (Rel. 35, Created)   |                 |         |
| DT         | 01-NOV-1997 (Rel. 35, Last sequence update)  |                 |         |
| DT         | 05-JUL-2004 (Rel. 44, Last annotation update)  |                 |         |
| DE         | Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor) (NPY5).  |                 |         |
| GN         | Name=NPY5R; Synonyms=NPYR5;  |                 |         |
| OS         | Homo sapiens (Human).  |                 |         |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                 |         |
| OC         | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |                 |         |
| OX         | NCBI_TaxID=9606;   |                 |         |
| RN         | [1]  |                 |         |
| RP         | SEQUENCE FROM N.A.   |                 |         |
| RC         | TISSUE=Hippocampus; PubMed=8700207;  |                 |         |
| RX         | MEDLINE=96317589; PubMed=8824284;  |                 |         |
| RA         | Batzl-Hartmann C., Walker M.W., Criscione L., Gustafson E.L.,  |                 |         |
| RA         | Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G.,   |                 |         |
| RA         | Taber R.I., Branchek T.A., Weinshank R.L.  |                 |         |
| RT         | "A receptor subtype involved in neuropeptide-Y-induced food intake."   |                 |         |
| RL         | Nature 382:168-171(1996).  |                 |         |
| RN         | [2]  |                 |         |
| RN         | SEQUENCE OF 11-455 FROM N.A.   |                 |         |
| RP         | MEDLINE=96421636; PubMed=8824284;  |                 |         |
| RX         | Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B.,   |                 |         |
| RA         | Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L.,  |                 |         |
| RA         | Sadlowski Y., Schaefer J., Velazquez N., McCaleb M.L.  |                 |         |
| RT         | "Identification of a novel hypothalamic neuropeptide Y receptor associated with feeding behavior."   |                 |         |
| RT         | J. Biol. Chem. 271:26315-26319(1996).  |                 |         |
| RN         | [3]  |                 |         |
| RN         | SEQUENCE OF 11-455 FROM N.A.   |                 |         |
| RP         | MEDLINE=9712686; PubMed=9169127;   |                 |         |
| RX         | Harzog H., Darby K., Ball H., Hort Y., Beck-Sickinger A., Shine J.,  |                 |         |
| RT         | "overlapping gene structure of the human neuropeptide Y receptor subtypes Y1 and Y5 suggests coordinate transcriptional regulation."   |                 |         |
| RL         | Genomics 41:315-319(1997).   |                 |         |
| RN         | [4]  |                 |         |
| RN         | SEQUENCE OF 11-455 FROM N.A.   |                 |         |
| RP         | Kopatz S.A., Aronstam R.S., Sharma S.V.,   |                 |         |
| RT         | "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."  |                 |         |
| RL         | Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.  |                 |         |
| CC         | -1- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylyate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders. |                 |         |
| CC         | -1- SUBCELLULAR LOCATION: Integral membrane protein.   |                 |         |
| CC         | -1- TISSUE SPECIFICITY: Brain; hypothalamus.   |                 |         |
| CC         | -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Highest to tachykinins receptors.  |                 |         |

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U56079; AAC50623.1; -  
 DR EMBL; U66275; AAC50741.1; -  
 DR EMBL; U94320; AAC51295.1; -  
 DR EMBL; AY322538; AAP84351.1; -  
 DR Genew; HGNC:7958; NPV5R.  
 DR MIM; 602001; -  
 DR GO; GO:000887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004983; F:neuropeptide Y receptor activity; TAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
 DR InterPro; IPR000276; GPCR Rhodopsn.  
 DR InterPro; IPR000393; NPV5\_receptor.  
 DR InterPro; IPR000611; NPV\_receptor.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECP F1.1; FALSE\_NEG.  
 DR PROSITE; PS0262; G-PROTEIN RECP F1.2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
 KW Phosphorylation; Transmembrane  
 FT DOMAIN 1 50 Extracellular (Potential).  
 FT TRANSMEM 51 72 1 (Potential).  
 FT DOMAIN 73 84 Cytoplasmic (Potential).  
 FT TRANSMEM 85 105 2 (Potential).  
 FT DOMAIN 106 125 Extracellular (Potential).  
 FT TRANSMEM 126 147 3 (Potential).  
 FT DOMAIN 148 167 Cytoplasmic (Potential).  
 FT TRANSMEM 168 188 4 (Potential).  
 FT DOMAIN 189 220 Extracellular (Potential).  
 FT TRANSMEM 221 242 5 (Potential).  
 FT DOMAIN 243 378 Cytoplasmic (Potential).  
 FT TRANSMEM 379 401 6 (Potential).  
 FT DOMAIN 402 418 Extracellular (Potential).  
 FT TRANSMEM 419 438 7 (Potential).  
 FT DOMAIN 439 455 Cytoplasmic (Potential).  
 FT CARBOHYD 20 20 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 27 27 N-linked (GlcNAc. . .) (Potential).  
 FT DISULFD 124 208 By similarity.  
 FT LIPID 452 452 S-palmitoyl cysteine (Potential).  
 SQ SEQUENCE 455 AA; 51990 MW; 95F2747E5F8F7 CRC64;

Query Match 100.0%; Score 2385; DB 1; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-150;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDEYNNKTLATENNNTAATRNDFPVWDYKSSVDDLYQFLIGLYTF 60  
 DB 1 MSFYSKQDYNMDELDEYNNKTLATENNNTAATRNDFPVWDYKSSVDDLYQFLIGLYTF 60  
 QY 61 VSLIGFVGNLLILMALMKRKNQKTVNPLIGNLAFSDILVFLFCSPPTLTSVLLDQWFG 120  
 DB 61 VSLIGFVGNLLILMALMKRKNQKTVNPLIGNLAFSDILVFLFCSPPTLTSVLLDQWFG 120  
 QY 121 KVMCHIMPFLQCVSLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGPAL 180  
 DB 121 KVMCHIMPFLQCVSLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGPAL 180  
 QY 181 CSPVPVHSLVELQETFGSALLSSRYLCVRSWPSDSYRIAFITSLLLVQVILPLVCLTVS 240  
 DB 181 CSPVPVHSLVELQETFGSALLSSRYLCVRSWPSDSYRIAFITSLLLVQVILPLVCLTVS 240  
 QY 241 HTSVCRSISGLNKENLRENEINILTLHPSKSGPOVKLSGSHKWSYFIKXRRYS 300  
 DB 241 HTSVCRSISGLNKENLRENEINILTLHPSKSGPOVKLSGSHKWSYFIKXRRYS 300  
 QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPPTCFEIKPENSDVHEL 360

DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPPTCFEIKPENSDVHEL 360  
 QY 361 RVKRSVTRIKRSRSEVRYLTILILPFAVSMPLHLFHVVTDFNDNLINRHKPLVYCIC 420  
 DB 361 RVKRSVTRIKRSRSEVRYLTILILPFAVSMPLHLFHVVTDFNDNLINRHKPLVYCIC 420  
 QY 421 HLLGMSSCCLNPLYGLFNNGIKADLVSLHCLHM 455  
 DB 421 HLLGMSSCCLNPLYGLFNNGIKADLVSLHCLHM 455

RESULT 2  
 AAH42416 PRELIMINARY; PRT; 445 AA.  
 ID AAH42416  
 AC AAH42416  
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Neuropeptide Y receptor Y5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC042416; AAH42416.1; -  
 KW Neuropeptide; Receptor.  
 SQ SEQUENCE 445 AA; 50726 MW; A2B0F3169DBA66BE CRC64;

Query Match 97.7%; Score 2330; DB 2; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-147;  
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYNNKTLATENNNTAATRNDFPVWDYKSSVDDLYQFLIGLYTFVSLIGFVGNL 70  
 DB 1 MDLEDEYNNKTLATENNNTAATRNDFPVWDYKSSVDDLYQFLIGLYTFVSLIGFVGNL 60  
 QY 71 LILMALMKRKNQKTVNPLIGNLAFSDILVFLFCSPPTLTSVLLDQWFGKVMCHIMPFL 130  
 DB 61 LILMALMKRKNQKTVNPLIGNLAFSDILVFLFCSPPTLTSVLLDQWFGKVMCHIMPFL 120  
 QY 131 QCVSVLSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGPALCSPLPVFHS 190  
 DB 121 QCVSVLSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGPALCSPLPVFHS 180

121 QCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTGLGFAICSPLPVPHSL 180  
191 VELQETFGSALLSSRYLCVESWSPDSYRIAFTISLLLVQVILPLVCLTVSHTSVCRSISC 250  
181 VELQETFGSALLSSRYLCVESWSPDSYRIAFTISLLLVQVILPLVCLTVSHTSVCRSISC 240  
251 GLSNKENRLEENEMINLTLPSSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 310  
241 GLSNKENRLEENEMINLTLPSSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 300  
311 ERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370  
301 ERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360  
371 KRSRSVFYELTILILVFAVSWMPHLFHVVTDFNDNLISNRHFKLVYCIHLLGWMSCCL 430  
361 KRSRSVFYELTILILVFAVSWMPHLFHVVTDFNDNLISNRHFKLVYCIHLLGWMSCCL 420  
431 NPILYGLNNGIKADLVSLIHCLHM 455  
421 NPILYGLNNGIKADLVSLIHCLHM 445

RESULT 4  
Q925F1 PRELIMINARY; PRT; 446 AA.  
ID Q925F1  
AC Q925F1  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE NP5 receptor 5.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184976; PubMed=11287090;  
RA Lundell I., Eriksson H., Matklund U., Larhammar D.;  
RT "Cloning and characterization of the guinea pig neuro peptide Y receptor Y5";  
RT Peptides 22:357-363(2001).  
RL Peptides 22:357-363(2001).  
DR EMBL; AF363240; AAK52800.1; --  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0004983; F: neuro peptide Y receptor activity; IEA.  
DR GO; GO:0004872; F: receptor activity; IEA.  
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P: G-protein coupled receptor protein signaling; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR000393; NP5\_receptor.  
DR InterPro; IPR000611; NP5\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PRINTS; PR01016; NRPEPTIDEYR.  
DR PRINTS; PR01012; NRPEPTIDEYR.  
DR PROSITE; PS50262; G\_PROTEIN\_RECIP\_F1\_2; 1.  
KW Neuro peptide; Receptor.  
SQ SEQUENCE 446 AA; 50936 MW; 2C3984B0A90AA693 CRC64;

Query Match 94.0%; Score 2241; DB 2; Length 446;  
Best Local Similarity 95.5%; Pred. No. 4.3e-141;  
Matches 425; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 11 MDLEDEYKTKLATENNTAATNSDFPVDDYKSSVDDLYFLIGLYTFVSLGFMGNL 70  
DB 1 MDLEDEYKTKLATENNTAATNSDFPVDDYKSSVDDLYFLIGLYTFVSLGFMGNL 60

QY 71 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLDQWFGKVMCHIMPEL 130  
DB 61 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLDQWFGKVMCHIMPEL 120

QY 131 QCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTGLGFAICSPLPVPHSL 190

191 VELQETFGSALLSSRYLCVESWSPDSYRIAFTISLLLVQVILPLVCLTVSHTSVCRSISC 250  
181 VELQETFGSALLSSRYLCVESWSPDSYRIAFTISLLLVQVILPLVCLTVSHTSVCRSISC 240  
251 GLSNKENRLEENEMINLTLPSSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 310  
241 GLSNKENRLEENEMINLTLPSSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 300  
311 ERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370  
301 ERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360  
371 KRSRSVFYELTILILVFAVSWMPHLFHVVTDFNDNLISNRHFKLVYCIHLLGWMSCCL 430  
361 KRSRSVFYELTILILVFAVSWMPHLFHVVTDFNDNLISNRHFKLVYCIHLLGWMSCCL 420  
431 NPILYGLNNGIKADLVSLIHCLHM 455  
421 NPILYGLNNGIKADLVSLIHCLHM 445

RESULT 3  
Q9GK73 PRELIMINARY; PRT; 445 AA.  
ID Q9GK73  
AC Q9GK73  
DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE Neuro peptide Y receptor Y5.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184974; PubMed=11287088;  
RA Gehlert D.R., Yang P., George C., Wang Y., Schober D.,  
RA Gackenheimer S., Johnson D., Beavers L.S., Gadske R.A., Baez M.;  
RT "Cloning and characterization of Rhesus monkey neuro peptide Y receptor subtypes (1)";  
RT Peptides 22:343-350(2001).  
RL Peptides 22:343-350(2001).  
DR EMBL; AF303091; AAG40773.1; --  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0004983; F: neuro peptide Y receptor activity; IEA.  
DR GO; GO:0004872; F: receptor activity; IEA.  
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007218; P: neuro peptide signaling pathway; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR000393; NP5\_receptor.  
DR InterPro; IPR000611; NP5\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PRINTS; PR01016; NRPEPTIDEYR.  
DR PRINTS; PR01012; NRPEPTIDEYR.  
DR PROSITE; PS50262; G\_PROTEIN\_RECIP\_F1\_2; 1.  
KW Neuro peptide; Receptor.  
SQ SEQUENCE 445 AA; 50812 MW; AEDACD2596758C93 CRC64;

Query Match 97.2%; Score 2318; DB 2; Length 445;  
Best Local Similarity 99.3%; Pred. No. 3.2e-146;  
Matches 442; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 MDLEDEYKTKLATENNTAATNSDFPVDDYKSSVDDLYFLIGLYTFVSLGFMGNL 70  
DB 1 MDLEDEYKTKLATENNTAATNSDFPVDDYKSSVDDLYFLIGLYTFVSLGFMGNL 60

QY 71 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLDQWFGKVMCHIMPEL 130  
DB 61 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLDQWFGKVMCHIMPEL 120

QY 131 QCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTGLGFAICSPLPVPHSL 190

Db 121 QCVSVLVSTLIIISIAIVRYHMKIPISNNLTANHGYFLIATVTLGLFAICSPLPVFFHSL 180  
 QY 191 VELQETFGSALLSSRYLCVSPDSYRIAFITISILLVQYILPLVCLTVSHTSVCRSISC 250  
 Db 181 VELQETFGSALLSSRYLCVSPDSYRIAFITISILLVQYILPLVCLTVSHTSVCRSISC 240  
 QY 251 GLSNKENRLEENEMINLTLPKSGQVQLSGSKWSPYFIKGRHRRYSKKTACVLPA 310  
 Db 241 GLSNKENRLEENEMINLTLPKSGQVQLSGSKWSPYFIKGRHRRYSKKTACVLPA 300  
 QY 311 ERPSQNHRSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370  
 Db 301 ARPSLENQSRTPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDAHEMRVRSITRIK 360  
 QY 371 KRSRSVYFVLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGMMSCCL 430  
 Db 361 KRSRSVYFVLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGMMSCCL 420  
 QY 431 NPILYGLFNNGIKADIVSLIHCLHM 455  
 Db 421 NPILYGLFNNGIKADIVSLIHCLHL 445

## RESULT 5

NYSR CANFA STANDARD; PRT; 446 AA.  
 AC 062729;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor) (NPY5)  
 DE Name=NPY5R; Synonyms=NPY5;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99017379; PubMed=9802393;  
 RA Borowsky B., Walker M.W., Bard J., Weinshank R.L., Laz T.M.,  
 RA Vaysses P., Branchek T.A., Gerald C.;  
 RA "Molecular biology and pharmacology of multiple NPY Y5 receptor species homologs";  
 RL Regul. Pept. 75:45-53(1998).  
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Highest to tachykinins receptors.  
 CC  
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 CC  
 CC EMBL; AF049328; AAC7838.1;  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC InterPro; IPR000393; NPY5\_Receptor.  
 CC InterPro; IPR000611; NPY\_Receptor.  
 CC Pfam; PF00001; 7tm1.1.  
 CC PRINTS; PR00237; GPCR\_Rhodopsn.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; FALSE\_NEG.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F2\_1;  
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation; Transmembrane.  
 FT DOMAIN 1 40 Extracellular (Potential).  
 FT TRANSMEM 41 62 1 (Potential).

FT DOMAIN 63 74 Cytoplasmic (Potential).  
 FT TRANSMEM 75 95 2 (Potential).  
 FT DOMAIN 96 115 Extracellular (Potential).  
 FT TRANSMEM 116 137 3 (Potential).  
 FT DOMAIN 138 157 Cytoplasmic (Potential).  
 FT TRANSMEM 158 178 4 (Potential).  
 FT DOMAIN 179 210 Extracellular (Potential).  
 FT TRANSMEM 211 232 5 (Potential).  
 FT DOMAIN 233 368 Cytoplasmic (Potential).  
 FT TRANSMEM 369 391 6 (Potential).  
 FT DOMAIN 392 404 Extracellular (Potential).  
 FT TRANSMEM 405 428 7 (Potential).  
 FT DOMAIN 429 446 Cytoplasmic (Potential).  
 FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 17 17 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 114 198 By similarity.  
 FT LIPID 442 442 S-palmitoyl cysteine (Potential).  
 SQ SEQUENCE 446 AA; 51012 MW; 5C8C8D2FC95D254A CRC64;

Query Match 93.4%; Score 2227; DB 1; Length 446;  
 Best Local Similarity 94.8%; Pred. NO. 3.7e-140;  
 Matches 422; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 11 MDLELDYNNKTLATENTTAATNSDFPVWDDYKSSVDDLOQYFLIGLYTFVSLFGMGNL 70  
 Db 1 MDLELDYNNKTLATENTTAATNSDFPVWDDYKSSVDDLOQYFLIGLYTFVSLFGMGNL 60  
 QY 71 LILMALMKRKNQKTVNFIIGNLAFSDILVLFCSPTLTSLVLLQDMFGKVMCHIMPFL 130  
 Db 61 LILMALMKRKNQKTVNFIIGNLAFSDILVLFCSPTLTSLVLLQDMFGKVMCHIMPFL 120  
 QY 131 QCVSVLVSTLIIISIAIVRYHMKIPISNNLTANHGYFLIATVTLGLFAICSPLPVFFHSL 190  
 Db 121 QCVSVLVSTLIIISIAIVRYHMKIPISNNLTANHGYFLIATVTLGLFAICSPLPVFFHSL 180  
 QY 191 VELQETFGSALLSSRYLCVSPDSYRIAFITISILLVQYILPLVCLTVSHTSVCRSISC 250  
 Db 181 VELQETFGSALLSSRYLCVSPDSYRIAFITISILLVQYILPLVCLTVSHTSVCRSISC 240  
 QY 251 GLSNKENRLEENEMINLTLPKSGQVQLSGSKWSPYFIKGRHRRYSKKTACVLPA 310  
 Db 241 GLSNKENRLEENEMINLTLPKSGQVQLSGSKWSPYFIKGRHRRYSKKTACVLPA 300  
 QY 311 ERPSQNHRSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370  
 Db 301 ARPSQNHRSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHDMRVRSIMRIK 360  
 QY 371 KRSRSVYFVLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGMMSCCL 430  
 Db 361 KRSRSVYFVLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGMMSCCL 420  
 QY 431 NPILYGLFNNGIKADIVSLIHCLHM 455  
 Db 421 NPILYGLFNNGIKADIVSLIHCLHM 445

## RESULT 6

NYSR RAT STANDARD; PRT; 456 AA.  
 AC 063634; P70586;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor).  
 DE Name=NPY5R; Synonyms=NPYR5;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;

RX MEDLINE=963117589; PubMed=8700207;  
RA Gerald C., Walker M.W., Criscione L., Gustafson E.L.,  
RA Batzl-Hartmann C., Smith K.E., Vayse P., Durkin M.M., Laz T.M.,  
RA Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G.,  
RA Taber R.I., Branche T.A., Weinshank R.L.;  
RT "A receptor subtype involved in neurotrophin-induced food intake.";  
RL Nature 382:168-171(1996).  
RN [2]  
RP SEQUENCE OF 12-456 FROM N.A.  
RX TISSUE=Brain;  
RX MEDLINE=98332165; PubMed=9669502;  
RA Parker E.M., Babi J.G., Balasubramanian A., Burrier R.E., Guzzi M.,  
RA Hamud F., Mukhopadhyay G., Rudinski M.S., Tao Z., Tice M., Xia L.,  
RA Mullins D.E., Salisbury B.G.;  
RT "G231118 (1129091) and other analogues of the C-terminus of  
neurotrophin Y are potent neurotrophin Y1 receptor antagonists and  
neurotrophin Y4 receptor agonists.";  
RL Eur. J. Pharmacol. 349:97-105(1998).  
RN [3]  
RP SEQUENCE OF 12-456 FROM N.A.  
RX STRAIN=Sprague-Dawley;  
RX MEDLINE=98421636; PubMed=8824284;  
RA Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B.,  
RA Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L.,  
RA Sadowski J., Schaefer J., Velazquez N., McCall M.L.;  
RT "Identification of a novel hypothalamic neurotrophin Y receptor  
associated with feeding behavior.";  
RL J. Biol. Chem. 271:26315-26319(1996).  
CC -!- FUNCTION: Receptor for neurotrophin Y and peptide YY. The activity  
of this receptor is mediated by G proteins that inhibit adenylyate  
cyclase activity. Seems to be associated with food intake. Could  
be involved in feeding disorders.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Brain; hypothalamus.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC Highest to tachykinin receptors.  
-----  
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DR EMBL; U56078; AAC52677.1; .  
DR EMBL; AF044264; AAC15670.1; .  
DR EMBL; U66274; AAC52845.1; .  
DR RGD; 3199; NPY5r.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR000393; NPY5\_receptor.  
DR InterPro; IPR000611; NPY\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; FALSE\_NEG.  
DR PROSITE; PS00462; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
KW Phosphorylation; Transmembrane.  
FT DOMAIN 1 51 Extracellular (Potential).  
FT TRANSMEM 52 73 1 (Potential).  
FT DOMAIN 74 85 Cytoplasmic (Potential).  
FT TRANSMEM 86 106 2 (Potential).  
FT DOMAIN 107 126 Extracellular (Potential).  
FT TRANSMEM 127 148 3 (Potential).  
FT DOMAIN 149 168 Cytoplasmic (Potential).  
FT TRANSMEM 169 189 4 (Potential).  
FT DOMAIN 190 221 Extracellular (Potential).  
FT TRANSMEM 222 243 5 (Potential).  
FT DOMAIN 244 278 Cytoplasmic (Potential).  
FT TRANSMEM 279 301 6 (Potential).  
FT DOMAIN 302 324 Extracellular (Potential).  
FT TRANSMEM 325 347 7 (Potential).  
FT DOMAIN 348 369 8 (Potential).  
FT TRANSMEM 370 392 9 (Potential).  
FT DOMAIN 393 415 10 (Potential).  
FT TRANSMEM 416 438 11 (Potential).  
FT DOMAIN 439 456 12 (Potential).

FT DISULFID 125 209 BY similarity.  
FT LIPID 452 S-palmitoyl cysteine (Potential).  
FT CARBOHYD 21 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 28 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 456 AA; 51715 MW; 5157ABE341BA707E CRC64;  
Query Match 87.4%; Score 2084.5; DB 1; Length 456;  
Best Local Similarity 88.2%; Pred. No. 1.1e-130;  
Matches 396; Conservative 22; Mismatches 30; Indels 1; Gaps 1;  
QY 7 QDYNMLELDEYNNKTLATENNATATRNDFPVDYDYSVDDLOVFLGLTYEVLGLF 66  
DB 8 QDSMEFLEEHFNKTFVTENNTAARNAAPFADYRGSVDDLOVFLGLTYEVLGLF 67  
QY 67 MGNLLILMALMKRNOKTTFNVLIGNLAFSDILVLFCSPPFTITSVLLDQWFGKVMCHI 126  
DB 68 MGNLLILMAVMKKNOKTTFNVLIGNLAFSDILVLFCSPPFTITSVLLDQWFGKVMCHI 127  
QY 127 MPFLQCVSVLSTLIILISIAIVRYHMKHPIINNLTANHGFLIATVWTGLFAICSLPV 186  
DB 128 MPFLQCVSVLSTLIILISIAIVRYHMKHPIINNLTANHGFLIATVWTGLFAICSLPV 187  
QY 187 FHSVLVELQETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCR 246  
DB 188 FHSVLVELQETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCR 247  
QY 247 SISCGLSNKENLEENEMINLTLPKSKGPGQVKGSGHWSYFPIKHHRRYSKKTACV 306  
DB 248 SISCGLSNKENLEENEMINLTLPKSKGPGQVKGSGHWSYFPIKHHRRYSKKTACV 307  
QY 307 LPAPERPSQENHSRIIPENFGSVRSOLSSSKFIPGVPTCFEIKPEENSDVHELVRKSV 366  
DB 308 LPAPERPSQENHSRIIPENFGSVRSOLSSSKFIPGVPTCFEIKPEENSDVHELVRKSV 366  
QY 367 TRIKRSRSVYFRTILILVFAVSMWPLHFLHVVTDFNDNLISNRHFKLVYICHLGLMM 426  
DB 367 TRIKRSRSVYFRTILILVFAVSMWPLHFLHVVTDFNDNLISNRHFKLVYICHLGLMM 426  
QY 427 SCCLNPLVGLFNGGKADLVSLHCLHM 455  
DB 427 SCCLNPLVGLFNGGKADLVSLHCLHM 455  
RESULT 7  
ID NY5R MOUSE STANDARD; PRT; 466 AA.  
AC O70342; O35380; Q9JMKJ;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5  
receptor).  
GN Name=Npy5r; Synonyms=Npy5;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98017379; PubMed=9802393;  
RA Borowsky B., Walker M.W., Bard J., Weinshank R.L., Laz T.M.,  
RA Vayse P., Branche T.A., Gerald C.;  
RT "Molecular biology and pharmacology of multiple NPY Y5 receptor  
species homologs.";  
RL Regul. Pept. 75:45-53(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=129/SV; TISSUE=Brain;  
RA Chen H., Adams S., McWhinnie E., Bayne M., Galski R., Zastawny R.;  
RT "Mouse neuropeptide Y Y5 receptor characterized by repeat sequence in  
extracellular domain.";  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97459646; PubMed=9315606; DOI=10.1016/S0005-2736(97)00131-4;  
 RA Nakamura M., Yokoyama M., Watanabe H., Matsumoto T.;  
 RT "Molecular cloning, organization and localization of the gene for the  
 RL mouse neurotrophin-3 receptor.";  
 CC Biochem. Biophys. Acta 1328:83-89(1997).  
 CC -!- FUNCTION: Receptor for neurotrophin-3 and peptide YY. The activity  
 CC of this receptor is mediated by G proteins that inhibit adenylyl-  
 CC cyclase activity. Seems to be associated with food intake. Could  
 CC be involved in feeding disorders (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC Highest to tachykinin receptors.  
 CC -----  
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 CC -----  
 CC EMBL; AF049329; AAC17839.1; -;  
 CC EMBL; AF022948; AAB81829.1; -;  
 CC EMBL; AB001346; EAA89538.1; -;  
 CC MGD; MGI:108082; Npy5r.  
 CC GO; GO:0016020; C:membrane; IDA.  
 CC GO; GO:001602; P:pamphatic polypeptide receptor activity; IDA.  
 CC GO; GO:0001601; P:peptide YY receptor activity; IDA.  
 CC GO; GO:0007273; P:regulation of synapse; IMP.  
 CC InterPro; IPR000276; GPCR\_Rhodpsn.  
 CC InterPro; IPR000393; NPV5\_Receptor.  
 CC InterPro; IPR000611; NPV\_Receptor.  
 CC Pfam; PF00001; 7tm1.1;  
 CC PRINTS; PR00237; GPCR\_Rhodopsin.  
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; FALSE\_NEG.  
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
 KW Phosphorylation; Transmembrane.  
 FT DOMAIN 1 61 Extracellular (Potential).  
 FT TRANSMEM 62 83 1 (Potential).  
 FT DOMAIN 84 95 Cytoplasmic (Potential).  
 FT TRANSMEM 96 116 2 (Potential).  
 FT DOMAIN 117 136 Extracellular (Potential).  
 FT TRANSMEM 137 158 3 (Potential).  
 FT DOMAIN 159 178 Cytoplasmic (Potential).  
 FT TRANSMEM 179 199 4 (Potential).  
 FT DOMAIN 200 231 Extracellular (Potential).  
 FT TRANSMEM 232 253 5 (Potential).  
 FT DOMAIN 254 388 Cytoplasmic (Potential).  
 FT TRANSMEM 389 411 6 (Potential).  
 FT DOMAIN 412 424 Extracellular (Potential).  
 FT TRANSMEM 425 448 7 (Potential).  
 FT DOMAIN 449 466 Cytoplasmic (Potential).  
 FT LIPID 467 462 S-palmitoyl cysteine (Potential).  
 FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 17 17 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 39 39 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 195 195 L -> F (in Ref. 1).  
 FT CONFLICT 284 284 K -> Q (in Ref. 3).  
 SQ SEQUENCE 466 AA; 52784 MW; B157F236EF2D4385 CRC64;

Query Match 86.8%; Score 2070; DB 1; Length 466;  
 Best Local Similarity 85.2%; Pred. No. 1.1e-129;  
 Matches 397; Conservative 23; Mismatches 24; Indels 22; Gaps 2;  
 QY 11 MDLEDEYKTLATENNAT-----RNSDFPVDYKGSVD 49  
 DB 1 MEVKLEHFNKFTVNTNNTAASQNTASPAWEDYRGTEENTSAARNTAFPPWEDYRGSVDD 60  
 QY 50 LQYFLIGLYTFVSLGLGFMGNLLILMAVMKKNQKTTVNFIGNLAFSDILVLFCSPPFL 109

DB 61 LQYFLIGLYTFVSLGLGFMGNLLILMAVMKKNQKTTVNFIGNLAFSDILVLFCSPPFL 120  
 QY 110 TSVLLQWFMFGKVMCHIMPFLQCVSVLSTLILSTAIYRYMIKHPISNNLTANHGYEL 169  
 DB 121 TSVLLQWFMFGKVMCHIMPFLQCVSVLSTLILSTAIYRYMIKHPISNNLTANHGYEL 180  
 QY 170 IATVTLGFAICSPLPVHSLVLEQTFGSAISSYLVCSWSPDSVRIATFISLLVQ 229  
 DB 181 IATVTLGFAICSPLPVHSLVLEQTFGSAISSYLVCSWSPDSVRIATFISLLVQ 240  
 QY 230 YILPLVCLTVSHTSVCSISCGLSNKENLENNMINLTLPSSKSGPGVKLSGSHKWSY 289  
 DB 241 YILPLVCLTVSHTSVCSISCGLSNKENLENNMINLTLPSSKSGPGVKLSGSHKWSY 300  
 QY 290 SFIKKRRYKSKTACVLPAPERPSQENHSRTLPENFGSVRSQSSSKFIPGVPTCFEI 349  
 DB 301 SFIKKRRYKSKTACVLPAPERPSQENHSRTLPENFGSVRSQSSSKFIPGVPTCFEI 359  
 QY 350 KPENSVDHELRYKRSVTRIKKRSRVFYRLTILILVFAVSWPLHLHFVHTDFDNLIS 409  
 DB 360 KPESSDAQEMRVKRSVTRIKKRSRVFYRLTILILVFAVSWPLHLHFVHTDFDNLIS 419  
 QY 410 NRHFKLVYICHLGGMSCCLNPILYGLNNGIKADLVSLHCLHM 455  
 DB 420 NRHFKLVYICHLGGMSCCLNPILYGLNNGIKADLVSLHCLHM 465  
 RESULT 8  
 BAC32426 PRELIMINARY; PRT; 466 AA.  
 ID BAC32426  
 AC BAC32426;  
 DT 14-APR-2004 (TrEMBLrel. 27, Created)  
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Adult male corpora quadrigemina cDNA, RIKEN full-length enriched  
 DE library, clone:B230213K17 product:NEUROPEPTIDE Y RECEPTOR TYPE 5, full  
 DE insert sequence.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RA "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RESULT 9  
NY5R PIG

Query Match 85.0%; Score 2028; DB 1; Length 446;  
 Best Local Similarity 85.4%; Pred. No. 6.4e-127; Mismatches 31; Indels 0; Gaps 0;  
 Matches 380; Conservative 34; Mismatches 31; Indels 0; Gaps 0;

QY 11 MDLEDEYNNKTLATENNNTAATRNDFPVMDDYKSSVDDLOQVFLIGLYTFVSLIGFMGNL 70  
 DB 1 MGSEIPDYNNKTLASENNNTVATNSGFPVWEDYKSSVDDLOQVFLIGLYTFVSLIGFMGNL 60  
 QY 71 LILMALMKRNQKTTVNFIGNLAFSDILVILVFCSPFTLTSLVLDQWFGKVMCHIMPFL 130  
 DB 61 LILMAVMKRNQKTTVNFIGNLAFSDILVILVFCSPFTLTSLVLDQWFGKVMCHIMPFL 120  
 QY 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAICSPLPVFHSL 190  
 DB 121 QCVTVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAICSPLPVFHSL 180  
 QY 191 VELOETFGSALSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 250  
 DB 181 VELOESFGSAWSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRITSC 240  
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYFPIKHHRRYSKKTACVLPAP 310  
 DB 241 GLSSQSKLEENEMINLTLPKAKRSGPAKLSHHPKWTYSFIRHHRRYSKKTACVLPAP 300  
 QY 311 ERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFPIKPEENSVDHVELRVKSVTRIK 370  
 DB 301 AGPALESREGRPPKVGSMQSPPPSNKFMFGVPTCFVPEKPEENSVDPEMVRSSIMRLR 360  
 QY 371 KRSRSVFRVRLTLLIIVFAVSNMPLHFLHVDTDFNDNLISNHFHKLVCICHLGWSGCC 430  
 DB 361 KRSRSVFRVRLTLLIIVFAVSNMPLHFLHVDTDFNDNLISNHFHKLVCICHLGWSGCC 420  
 QY 431 NPILYGLNNGIKADLVSLIHLCHM 455  
 DB 421 NPILYGLNNGIKADLVSLIHLCHV 445

## RESULT 10

QSQFM2 ID QSQFM2 PRELIMINARY; PRT; 443 AA.  
 AC QSQFM2;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Neuropeptide Y receptor Y5.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Holmberg S.K.S.; Mikko S.; Boswell T.; Zoorob R.; Latham D.;  
 RT "Pharmacological characterization of cloned chicken neuropeptide Y  
 receptors Y1 and Y5."  
 RL J. Neurochem. 0:0-0(2003).  
 DR EMBL; AY040844; AAK83556.1;  
 DR GO; GO:0046021; C:integral to membrane; IEA.  
 DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR000393; NPY5\_Receptor.  
 DR InterPro; IPR000611; NPY5\_Receptor.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PRINTS; PR01016; NREPTIDEY5R.  
 DR PRINTS; PR01012; NREPTIDEYR.  
 DR PROSITE; PS0262; G.PROTEIN\_RECEP\_F1\_2; 1.  
 KW Neuropeptide; Receptor  
 SQ SEQUENCE 443 AA; 50044 MW; EFE9FLA391CC0925 CRC64;

Query Match 68.3%; Score 1629.5; DB 2; Length 443;  
 Best Local Similarity 70.0%; Pred. No. 2.1e-100; Mismatches 51; Indels 5; Gaps 4;  
 Matches 310; Conservative 51; Mismatches 77; Indels 5; Gaps 4;

QY 11 MDLEDEYNNKTLATENNNTAATRNDFPVMDDYKSSVDDLOQVFLIGLYTFVSLIGFMGNL 70  
 DB 1 MDLGFQDYNNKTLATENNNTAATRNDFPVMDDYKSSVDDLOQVFLIGLYTFVSLIGFMGNL 57  
 QY 71 LILMALMKRNQKTTVNFIGNLAFSDILVILVFCSPFTLTSLVLDQWFGKVMCHIMPFL 130  
 DB 58 LVLTLAL-TKRQKQTTINILIGNLAFSDILVILVFCSPFTLTSLVLDQWFGKVMCHIMPFL 116  
 QY 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAICSPLPVFHSL 190  
 DB 117 QCVTVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAICSPLPVFHSL 176  
 QY 191 VELOETFGSALSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 250  
 DB 177 VDLRKTINLEALENRLLCIESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 236  
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYFPIKHHRRYSKKTACVLPAP 310  
 DB 237 RUSSKEGKFOENEMINLTLPKSKAGTEAOPSHTSWSCALVRKHRRYSKKTSTVMPAI 296  
 QY 311 ERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFPIKPEENSVDHVE-LRVKRSVTRI 369  
 DB 297 LRQQQADFRDLPTSGTEKSQLSSSKFIPGVPTCFEMKPEENTEIQDMITVSQSIIRI 356  
 QY 370 KRSRSVFRVRLTLLIIVFAVSNMPLHFLHVDTDFNDNLISNHFHKLVCICHLGWSGCC 429  
 DB 357 KRSRSVFRVRLTLLIIVFAVSNMPLHFLHVDTDFNDNLISNHFHKLVCICHLGWSGCC 416  
 QY 430 NPILYGLNNGIKADLVSLIHLCH 452  
 DB 417 NPILYGLNNGIKADLVSLIHLCH 439

## RESULT 11

073733 ID 073733 PRELIMINARY; PRT; 377 AA.  
 AC 073733;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Neuropeptide Y/peptide YY receptor Ya.  
 GN Names=NPYra; Synonyms=NPYRYA;  
 OS Brachydanio rerio (Zebrafish). (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lundell I.; Berglund M.M.; Starback P.; Salaneck E.; Gehlert D.R.;  
 RA Larhammar D.;  
 RT "Cloning and characterization of a novel neuropeptide Y receptor  
 subtype in the zebrafish."  
 RL DNA Cell Biol. 16:1357-1363 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ringvall M.; Berglund M.M.; Larhammar D.;  
 RT "Multiplicity of neuropeptide Y receptors: cloning of a third distinct  
 subtype in the zebrafish."  
 RL Biochem. Biophys. Res. Commun. 241:749-755 (1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Starback P.; Lundell I.; Fredriksson R.; Berglund M.M.; Yan Y.L.;  
 RA Wraith A.; Soderberg C.; Postlethwait J.H.; Larhammar D.;  
 RT "Neuropeptide Y receptor subtype with unique properties cloned in the  
 zebrafish: the zya receptor."



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RL Brain Res. Mol. Brain Res. 70:242-252 (1999).
DR EMBL; AF037400; AAC41276.1; -.
DR ZFIN; ZDB-GENE-980526-393; npy1ya.
DR GO; GO:016021; C:integral to membrane; IEA.
DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007218; F:neuropeptide signaling pathway; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000351; NP1L_Receptor.
DR InterPro; IPR000611; NP1L_Receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01013; NP1L_Receptor.
DR PRINTS; PR01012; NP1L_Receptor.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR Neuropeptide; Receptor.
SQ SEQUENCE 377 AA; 42901 MW; 60562AD9C7BF5D0 CRC64;

Query Match 23.4%; Score 558; DB 2; Length 377;
Best Local Similarity 28.5%; Pred. No. 3.4e-29;
Matches 124; Conservative 68; Mismatches 136; Indels 106; Gaps 6;

QY 20 NKTATENNATATNSDPFVDDYKSSVDDIQLYFLIGLYTFVSLGLFVGNLLIMALKK 79
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
16 NSTLTHNQNSLFLDPCW--QSTWTLT--LVLCYCLVLILGLLGNILLICIIMHQ 70
QY 80 RQKTTWFLNGLAFSDILVLFCSPTLTSVLLDQWFGKVMCHMPFQCVSVLST 139
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
71 RPPNVTSLIANLSVSDILSVFCLPTVTVTLNDHWIFGALLCRLMPFQCVSVTVSV 130
QY 140 LILISIAIVRYMKHPIISNNJTAHGYFLIATVTLGFAICSPLPVPHSLVELQETFGS 199
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
131 LSLVIALERHQLLHPGSKVSPQAVIATVTLACVTSPLPFLAFHLITSPYSLFP 190
QY 200 ALLSSRYLCVSPSDSVRIATISLLVQVILPLVCLTVSHTSVCRSISGLSKENRL 259
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 APLSQLQVCLVWPQDQKLAATTSLLFQCCPLLMLLCYLI----- 235
QY 260 ENEMINLTLPSSKSGPOVKLSGSHKWSYGIKRRRYSKKTACVLPAPERESQNH 319
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
236 -----FLRQRERMLERQC-----SRNREDEHR 259
QY 320 RILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHRLVRKSVTRIKRSRVSFYR 379
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
260 RVN-----HSKRINVM 270
QY 380 LTILILVFAVSWPLHLPHVVTDFDNDNLISNRHFKLVYICICHLGMMSCCLNPILYGLN 439
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
271 LATLVAAFAVCWLPNAFNWADCDQEVLPVCNHNLLFSLCHLLANSSTCVNPIIYGLN 330
QY 440 NGTKADLVSLI-RC 452
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
331 SNFRKDVASVVLHC 344

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RA Salaneck E., Ardell D.H., Larson E.T., Larhammar D.;
RT "Three neuropeptide Y receptor genes in the spiny dogfish, Squalus
RT acanthias, support en bloc duplications in early vertebrate
RL Mol. Biol. Evol. 20:1271-1280(2003).
RN [2].
RP SEQUENCE FROM N.A.
RA Salaneck E.W., Larson E.T., Ardell D.H., Larhammar D.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY177273; AAC62565.1; -.
DR EMBL; AV177272; AAC62565.1; JOINED.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000351; NP1L_Receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01013; NP1L_Receptor.
DR PRINTS; PR01012; NP1L_Receptor.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 348
SQ SEQUENCE 348 AA; 40738 MW; 817D35C3DAFD90F CRC64;

Query Match 25.1%; Score 527; DB 2; Length 348;
Best Local Similarity 25.7%; Pred. No. 3.6e-27;
Matches 115; Conservative 79; Mismatches 122; Indels 132; Gaps 7;

QY 5 SKQDYNMDELDVYNNKTATNTATNSDPFVDDYKSSVDDIQLYFLIGLYTFVSL 64
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
19 SERNTLD-NYDQCSQTA-----MIPTLALYSAIL 51
QY 65 GFMGNLLITMALKRCKTTFNFIAGLAFSDILVLFCSPTLTSVLLDQWFGKVMC 124
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
52 GVSNGNLLITIMKQENHNTNLIYNLSVSDILSVMLPFTLVTFDHWIFGSANC 111
QY 125 HMPFLQCVSVLSTLILISIAIVRYMKHPIISNNJTAHGYFLIATVTLGFAICSP 184
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
112 KLSNMIQCSITSVSIFSLVIAVERHQLIINPQGRPNKHAVLSIVTMWTLALLTSLPF 171
QY 185 PVFHSVLVELQETFG-SALLSSRYLCVSPSDSVRIATISLLVQVILPLVCLTVSHTS 243
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
172 LILFNLTDQVPHGYSYTFEAGKYNCLQWFSQVSETQVLYTTCLLVQVYFALCFICYFK 231
QY 244 VCRSISGLSKENRLEENEMINLTLPSSKSGPOVKLSGSHKWSYGIKRRRYSKKT 303
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
232 I-----YILRRRNTM-- 243
QY 304 ACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHRLVK 363
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
244 -----DKREEN-----KYPADEN----- 257
QY 364 RSVTRIKRSRVSFVRLTILVFAVSWPLHLPHVVTDFDNDNLISNRHFKLVYICICHL 423
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
258 -----RRINIMLISIVVAFAICWLPINFAVDFWNEVYINNCHNLVFSICHLT 307
QY 424 GMMSCCLNPILYGLNNGIKADLVSLIH 451
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
308 AMLSTCTNPITYGLNKNFQDLRSILH 335

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## RESULT 13

AAO62565

ID AAO62565 PRELIMINARY; PRT; 348 AA.

DT 25-MAR-2004 (TREMELrel. 27, Created)

DT 25-MAR-2004 (TREMELrel. 27, Last sequence update)

DE NPY receptor Y1 (fragment).

OS Squalus acanthias (Spiny dogfish).

RX

SEQUENCE FROM N.A.

MEDLINE=22763539; PubMed=12777532;



Search completed: October 21, 2004, 12:13:17  
Job time : 193 secs





Db 1 MSFYSKQDYNMDELDEYNNKTATNTAATNSDFPVDYKSSVDDLOFLGLYTF 60  
 QY 61 VSLGPMGNLLIIMALKRKNQKTTNFIIGNLAFSDILVLFCSPTLTSLVLLDQWFG 120  
 Db 61 VSLGPMGNLLIIMALKRKNQKTTNFIIGNLAFSDILVLFCSPTLTSLVLLDQWFG 120  
 QY 121 KVMCHIMPFLQCVSVLVSTLIIISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180  
 Db 121 KVMCHIMPFLQCVSVLVSTLIIISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180  
 QY 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
 Db 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
 QY 241 HTSVCRSISCGLSNKENLEENEMINLTLPSPKSGPQVKLSGSHKWSYFIKHHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENLEENEMINLTLPSPKSGPQVKLSGSHKWSYFIKHHRRYS 300  
 QY 301 KKTACVLPAPERPSOENHSRIILPENFGSVRSQSSSKFIPOVPTCFEIKPEENSVDVHEL 360  
 Db 301 KKTACVLPAPERPSOENHSRIILPENFGSVRSQSSSKFIPOVPTCFEIKPEENSVDVHEL 360  
 QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 Db 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 QY 421 HLLGMMSCCLNPILYGLFNNNGIKADLVSLIHCLHM 455  
 Db 421 HLLGMMSCCLNPILYGLFNNNGIKADLVSLIHCLHM 455

RESULT 2

US-08-566-096A-4  
 ; Sequence 4, Application US/08566096A  
 ; Patent No. 5968819  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerald, Christophe P.G.  
 ; APPLICANT: Walker, Mary W.  
 ; APPLICANT: Branchek, Theresa  
 ; APPLICANT: Weinshank, Richard L.  
 ; TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR.  
 ; TITLE OF INVENTION: COMPOUNDS USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC  
 ; TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (YS) AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: United States of America  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/566,096A  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 1795/46166-B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 278-0400  
 ; TELEFAX: (212) 391-0525  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 455 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

US-08-566-096A-4

Query Match 100.0%; Score 2385; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred No. 5,3e-180;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSFYSKQDYNMDELDEYNNKTATNTAATNSDFPVDYKSSVDDLOFLGLYTF 60  
 Db 1 MSFYSKQDYNMDELDEYNNKTATNTAATNSDFPVDYKSSVDDLOFLGLYTF 60  
 QY 61 VSLGPMGNLLIIMALKRKNQKTTNFIIGNLAFSDILVLFCSPTLTSLVLLDQWFG 120  
 Db 61 VSLGPMGNLLIIMALKRKNQKTTNFIIGNLAFSDILVLFCSPTLTSLVLLDQWFG 120  
 QY 121 KVMCHIMPFLQCVSVLVSTLIIISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180  
 Db 121 KVMCHIMPFLQCVSVLVSTLIIISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180  
 QY 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
 Db 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
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 Db 241 HTSVCRSISCGLSNKENLEENEMINLTLPSPKSGPQVKLSGSHKWSYFIKHHRRYS 300  
 QY 301 KKTACVLPAPERPSOENHSRIILPENFGSVRSQSSSKFIPOVPTCFEIKPEENSVDVHEL 360  
 Db 301 KKTACVLPAPERPSOENHSRIILPENFGSVRSQSSSKFIPOVPTCFEIKPEENSVDVHEL 360  
 QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 Db 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 QY 421 HLLGMMSCCLNPILYGLFNNNGIKADLVSLIHCLHM 455  
 Db 421 HLLGMMSCCLNPILYGLFNNNGIKADLVSLIHCLHM 455

RESULT 3

US-08-668-650B-4  
 ; Sequence 4, Application US/08668650B  
 ; Patent No. 5989920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerald, Christophe P.G.  
 ; APPLICANT: Walker, Mary W.  
 ; APPLICANT: Branchek, Theresa  
 ; APPLICANT: Weinshank, Richard L.  
 ; TITLE OF INVENTION: Methods of Modifying Feeding Behavior,  
 ; TITLE OF INVENTION: Compounds Useful in Such Methods, And DNA Encoding a  
 ; TITLE OF INVENTION: Hypothalamic Atypical Neuropeptide Y/Peptide YY Receptor  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/668,650B  
 ; FILING DATE: 04-JUN-1996  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White Esq., John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 1795/46166C

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-278-0400  
 TELEFAX: 212-391-0525  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 455 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-668-650B-4

Query Match 100.0%; Score 2385; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-180;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60  
 DB 1 MSFYSKQDYNMDELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60

QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWMPG 120  
 DB 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWMPG 120

QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180  
 DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180

QY 181 CSPLPVFHSLVELQETFGSALLSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
 DB 181 CSPLPVFHSLVELQETFGSALLSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPKSKGQVKSGLSHKWSYFIKKHRRYS 300  
 DB 241 HTSVCRSISCGLSNKENLEENEMINTLHPKSKGQVKSGLSHKWSYFIKKHRRYS 300

QY 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360  
 DB 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360

QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNWPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 DB 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNWPLHLFHVVTDFNDNLISNRHFKLVYCIC 420

QY 421 HLLGMSCCLNPILYGLFNNNGIKADLVSLIHCLHM 455  
 DB 421 HLLGMSCCLNPILYGLFNNNGIKADLVSLIHCLHM 455

RESULT 4  
 US-09-200-673-4  
 Sequence 4, Application US/09200673A  
 Patent No. 6316203

GENERAL INFORMATION:  
 APPLICANT: Gerald, Christophe P.G.  
 APPLICANT: Weinschank, Richard L.  
 APPLICANT: Walker, Mary W.  
 APPLICANT: Branchek, Theresa  
 TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful  
 TITLE OF INVENTION: In Such Methods, and DNA Encoding A Hypothalamic  
 TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (Y5)  
 FILE REFERENCE: 46166-BZ/JPW  
 CURRENT APPLICATION NUMBER: US/09/200,673A  
 CURRENT FILING DATE: 1998-11-25  
 EARLIER APPLICATION NUMBER: 08/566,096  
 EARLIER FILING DATE: 1995-12-01  
 EARLIER APPLICATION NUMBER: 08/349,025  
 EARLIER FILING DATE: 1994-12-02  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 455  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-09-200-673-4

Query Match 100.0%; Score 2385; DB 3; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-180;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60  
 DB 1 MSFYSKQDYNMDELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60

QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWMPG 120  
 DB 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWMPG 120

QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180  
 DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180

QY 181 CSPLPVFHSLVELQETFGSALLSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240  
 DB 181 CSPLPVFHSLVELQETFGSALLSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPKSKGQVKSGLSHKWSYFIKKHRRYS 300  
 DB 241 HTSVCRSISCGLSNKENLEENEMINTLHPKSKGQVKSGLSHKWSYFIKKHRRYS 300

QY 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360  
 DB 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360

QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNWPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 DB 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNWPLHLFHVVTDFNDNLISNRHFKLVYCIC 420

QY 421 HLLGMSCCLNPILYGLFNNNGIKADLVSLIHCLHM 455  
 DB 421 HLLGMSCCLNPILYGLFNNNGIKADLVSLIHCLHM 455

RESULT 5

US-09-194-895-4  
 Sequence 4, Application US/09194895  
 Patent No. 6531287

GENERAL INFORMATION:  
 APPLICANT: Gerald, Christophe P.G.  
 APPLICANT: Weinschank, Richard L.  
 APPLICANT: Walker, Mary M  
 APPLICANT: Branchek, Theresa  
 TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful  
 TITLE OF INVENTION: In Such Methods and DNA Encoding A Hypothalamic  
 TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (Y5)  
 FILE REFERENCE: 1795-46166-D-PCT-US/JPW/BJA  
 CURRENT APPLICATION NUMBER: US/09/194,895  
 CURRENT FILING DATE: 1999-09-27  
 PRIOR APPLICATION NUMBER: PCT/US97/09504  
 PRIOR FILING DATE: 1997-06-04  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 455  
 TYPE: PRT  
 ORGANISM: Homo sapiens

Query Match 100.0%; Score 2385; DB 4; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-180;  
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60  
 DB 1 MSFYSKQDYNMDELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60

QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWMPG 120

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Db      61 VSLGFMGNLLILMALMKRQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQMFG 120
QY      121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
Db      121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
QY      181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Db      181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
QY      241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKHHRRYS 300
Db      241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKHHRRYS 300
QY      301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQVPTCFEIKPEENSVDVHEL 360
Db      301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQVPTCFEIKPEENSVDVHEL 360
QY      361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Db      361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
QY      421 HLLGWMSCCLNPILYGFLLNGIKADLVSLIHCLEM 455
Db      421 HLLGWMSCCLNPILYGFLLNGIKADLVSLIHCLEM 455

```

## RESULT 6

US-10-013-846-7

; Sequence 7, Application US/10013846

; Patent No. 6566367

; GENERAL INFORMATION:

; APPLICANT: Bakhtavachalam, Rajagopal

; APPLICANT: Blum, Charles A

; APPLICANT: Briemann, Harry L

; APPLICANT: Darrow, James W

; APPLICANT: De Lombaert, Stephane

; APPLICANT: Hutchison, Alan

; APPLICANT: Tran, Jennifer

; APPLICANT: Zheng, Xiaozhang

; APPLICANT: Elliott, Richard L

; APPLICANT: Hammond, Marys

; TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and

; FILE REFERENCE: N00.2001

; CURRENT APPLICATION NUMBER: US/10/013,846

; PRIOR FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: US 60/254,990

; PRIOR FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 455

; TYPE: PRT

; ORGANISM: homosapiens

US-10-013-846-7

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Query Match      100.0%; Score 2385; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.3e-180;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MSFYSKQDYNMDELDEYYNKTLATENNNTAATRSDFPVDYKSSVDDIQYFLIGLYTF 60
Db      1 MSFYSKQDYNMDELDEYYNKTLATENNNTAATRSDFPVDYKSSVDDIQYFLIGLYTF 60
QY      61 VSLGFMGNLLILMALMKRQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQMFG 120
Db      61 VSLGFMGNLLILMALMKRQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQMFG 120
QY      121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
Db      121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180

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QY      181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Db      181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
QY      241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKHHRRYS 300
Db      241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKHHRRYS 300
QY      301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQVPTCFEIKPEENSVDVHEL 360
Db      301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQVPTCFEIKPEENSVDVHEL 360
QY      361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Db      361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
QY      421 HLLGWMSCCLNPILYGFLLNGIKADLVSLIHCLEM 455
Db      421 HLLGWMSCCLNPILYGFLLNGIKADLVSLIHCLEM 455

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## RESULT 7

US-09-447-907-4

; Sequence 4, Application US/09447907

; Patent No. 6645774

; GENERAL INFORMATION:

; APPLICANT: Gerald, Christophe P.G.

; APPLICANT: Weinshank, Richard L

; APPLICANT: Walker, Mary W

; APPLICANT: Brancheck, Theresa

; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful in Such Me

; FILE REFERENCE: 1795-46166CA

; CURRENT APPLICATION NUMBER: US/09/447,907

; CURRENT FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: 08/668,650

; PRIOR FILING DATE: 1996-06-04

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 455

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Human Y5 cDNA clone

US-09-447-907-4

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Query Match      100.0%; Score 2385; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.3e-180;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MSFYSKQDYNMDELDEYYNKTLATENNNTAATRSDFPVDYKSSVDDIQYFLIGLYTF 60
Db      1 MSFYSKQDYNMDELDEYYNKTLATENNNTAATRSDFPVDYKSSVDDIQYFLIGLYTF 60
QY      61 VSLGFMGNLLILMALMKRQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQMFG 120
Db      61 VSLGFMGNLLILMALMKRQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQMFG 120
QY      121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
Db      121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
QY      181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Db      181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
QY      241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKHHRRYS 300
Db      241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKHHRRYS 300
QY      301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQVPTCFEIKPEENSVDVHEL 360

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Db 301 KKTACVLPAERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL 360  
QY 361 RVKRSVTRIKRSRSVFRYLITILVFAVSWMPHLFHVVTDFNDNLISNRHFKLYCIC 420  
Db 361 RVKRSVTRIKRSRSVFRYLITILVFAVSWMPHLFHVVTDFNDNLISNRHFKLYCIC 420  
QY 421 HLLGWSCLNPILYGFLLNGIKADLVSLIHCLHM 455  
Db 421 HLLGWSCLNPILYGFLLNGIKADLVSLIHCLHM 455  
RESULT 8  
PCT-US95-15646-4  
; Sequence 4, Application PC/TUS9515646  
; GENERAL INFORMATION:  
; APPLICANT: Syntactic Pharmaceutical Corporation  
; TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR, COMPOUNDS  
; TITLE OF INVENTION: USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC ATYPIC  
; TITLE OF INVENTION: Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/15646  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 1795/46166-A-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 456 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-15646-4  
Query Match 100.0%; Score 2385; DB 5; Length 456;  
Best Local Similarity 100.0%; Pred. No. 5.4e-180;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSFYKQDYNMDELYNKTATNTAATRNDDYKSSVDDLOVFLGLTYF 60  
Db 1 MSFYKQDYNMDELYNKTATNTAATRNDDYKSSVDDLOVFLGLTYF 60  
QY 61 VLLGFMGNLLIIMALKKRNOKTTVFNFLGNLAFSDILVLFCSPTLTSVLLDQWMFG 120  
Db 61 VLLGFMGNLLIIMALKKRNOKTTVFNFLGNLAFSDILVLFCSPTLTSVLLDQWMFG 120  
QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGFIATVTLGFAI 180  
Db 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGFIATVTLGFAI 180  
QY 181 CSPLPVHSLVELQETFGGALLSSRYLCVESPSSSYRAFTISLLVQYILPLVCLTVS 240  
Db 181 CSPLPVHSLVELQETFGGALLSSRYLCVESPSSSYRAFTISLLVQYILPLVCLTVS 240  
QY 241 HTSVCRSISGLSNKENLEENEMINLTLPKSKGPGVKLSGSHKWSYFIKKHRRYS 300

Db 241 HTSVCRSISGLSNKENLEENEMINLTLPKSKGPGVKLSGSHKWSYFIKKHRRYS 300  
QY 301 KKTACVLPAERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL 360  
Db 301 KKTACVLPAERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL 360  
QY 361 RVKRSVTRIKRSRSVFRYLITILVFAVSWMPHLFHVVTDFNDNLISNRHFKLYCIC 420  
Db 361 RVKRSVTRIKRSRSVFRYLITILVFAVSWMPHLFHVVTDFNDNLISNRHFKLYCIC 420  
QY 421 HLLGWSCLNPILYGFLLNGIKADLVSLIHCLHM 455  
Db 421 HLLGWSCLNPILYGFLLNGIKADLVSLIHCLHM 455  
RESULT 9  
US-08-630-118A-5  
; Sequence 6, Application US/08630118A  
; Patent No. 5919901  
; GENERAL INFORMATION:  
; APPLICANT: Hu Ph.D., Yinghe  
; APPLICANT: McCaleb Ph.D., Michael L.  
; APPLICANT: Bloomquist Ph.D., Brian T.  
; APPLICANT: Flores-Riveros Ph.D., Jaime R.  
; APPLICANT: Cornfield Ph.D., Linda J.  
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
; TITLE OF INVENTION: Sequences  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,118A  
; FILING DATE: April 8, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greenfield Ph.D., Michael S.  
; REGISTRATION NUMBER: 37,142  
; REFERENCE/DOCKET NUMBER: 96,149/WH 405  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 715-1000  
; TELEFAX: (312) 715-1234  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-630-118A-6  
Query Match 97.7%; Score 2330; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 1.1e-175;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 MDLEDDYNNKLTATNTAATRNDDYKSSVDDLOVFLGLTYFVSLIGFNGNL 70  
Db 1 MDLEDDYNNKLTATNTAATRNDDYKSSVDDLOVFLGLTYFVSLIGFNGNL 60  
QY 71 LILMALMKRNOKTTVFNFLGNLAFSDILVLFCSPTLTSVLLDQWMFGKVMCHIMPFL 130  
Db 61 LILMALMKRNOKTTVFNFLGNLAFSDILVLFCSPTLTSVLLDQWMFGKVMCHIMPFL 120  
QY 131 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGFIATVTLGFAICSPLPVHSL 190

Db 121 QCVSVLSTLILISIAIVRYHMKHPISSNNLTANHGFLIATVWTLGFAICSPLPVHSL 180  
QY 191 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISILLVOYIILPLVCLTVSHTSVCRSISC 250  
Db 181 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISILLVOYIILPLVCLTVSHTSVCRSISC 240  
QY 251 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFPIKRRRYRYKKTACVLPAP 310  
Db 241 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFPIKRRRYRYKKTACVLPAP 300  
QY 311 ERPSQENHGRILPENFGSVRSQSSSKPIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370  
Db 301 ERPSQENHGRILPENFGSVRSQSSSKPIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360  
QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 430  
Db 361 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 420  
QY 431 NPILYGLFNNGIKADLVSLIHCLHM 455  
Db 421 NPILYGLFNNGIKADLVSLIHCLHM 445

## RESULT 10

US-08-838-399-6  
; Sequence 6, Application US/08838399  
; Patent No. 5965392  
; GENERAL INFORMATION:  
; APPLICANT: Hu Ph.D., Yinghe  
; APPLICANT: McCaleb Ph.D., Michael L.  
; APPLICANT: Bloomquist Ph.D., Brian T.  
; APPLICANT: Flores-Riveros Ph.D., Jaime R.  
; APPLICANT: Cornfield Ph.D., Linda J.  
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838.399  
; FILING DATE:  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
; NAME: Greenfield Ph.D., Michael S.  
; REGISTRATION NUMBER: 37,147  
; REFERENCE/DOCKET NUMBER: 96,149/WH 405  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 715-1000  
; TELEFAX: (312) 715-1234  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-838-399-6  
Query Match 97.7%; Score 2330; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 1.1e-175;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDLELDYVYKTLATENTNATNSDFPWDDYKSSVDDLQYFLIGLYTFVSLGFMGNL 60  
QY 71 LILMALMKKNQKTTNVNFLIGNLAFSDILVLFCSPTTLTSVLLDQWFGKVMCHIMPFL 130  
Db 61 LILMALMKKNQKTTNVNFLIGNLAFSDILVLFCSPTTLTSVLLDQWFGKVMCHIMPFL 120  
QY 131 QCVSVLSTLILISIAIVRYHMKHPISSNNLTANHGFLIATVWTLGFAICSPLPVHSL 190  
Db 121 QCVSVLSTLILISIAIVRYHMKHPISSNNLTANHGFLIATVWTLGFAICSPLPVHSL 180  
QY 191 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISILLVOYIILPLVCLTVSHTSVCRSISC 250  
Db 181 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISILLVOYIILPLVCLTVSHTSVCRSISC 240  
QY 251 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFPIKRRRYRYKKTACVLPAP 310  
Db 241 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFPIKRRRYRYKKTACVLPAP 300  
QY 311 ERPSQENHGRILPENFGSVRSQSSSKPIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370  
Db 301 ERPSQENHGRILPENFGSVRSQSSSKPIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360  
QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 430  
Db 361 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 420  
QY 431 NPILYGLFNNGIKADLVSLIHCLHM 455  
Db 421 NPILYGLFNNGIKADLVSLIHCLHM 445

## RESULT 11

US-09-003-199-21  
; Sequence 21, Application US/09003199  
; Patent No. 5985616  
; GENERAL INFORMATION:  
; APPLICANT: Parker, Eric M  
; APPLICANT: Strader, Catherine D  
; APPLICANT: Rudinski, Mark S  
; TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schering-Plough Corporation  
; STREET: 2000 Galloping Hill Road  
; CITY: Kenilworth  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07033-0530  
; MEDIUM TYPE: Diskette  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.5.3  
; SOFTWARE: Microsoft Word 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,199  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thampoe, Immac J.  
; REGISTRATION NUMBER: 36,322  
; REFERENCE/DOCKET NUMBER: CN0775  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 298-5061  
; TELEFAX: (908) 298-5388  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-003-199-21

QY 11 MDLELDYVYKTLATENTNATNSDFPWDDYKSSVDDLQYFLIGLYTFVSLGFMGNL 70

Query Match 97.7%; Score 2330; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 1.1e-175;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 MDLEDEYNNKTLATENNNTAATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 70  
1 MDLEDEYNNKTLATENNNTAATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 60

71 LILMALMKRNOKTTNVLNGLAFSDILVLFCSPTLTSVLLDQWFMGKVMCHIMPFL 130  
61 LILMALMKRNOKTTNVLNGLAFSDILVLFCSPTLTSVLLDQWFMGKVMCHIMPFL 120

131 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAICSLPVFHS 190  
121 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAICSLPVFHS 180

191 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQVILPLVCLTVSHTSVCRSISC 250  
181 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQVILPLVCLTVSHTSVCRSISC 240

251 GLSNKENRLEENEMINLTLPKSKGQVQLSGSHKWSYFIKRRRRYSKKTACVLPAP 310  
241 GLSNKENRLEENEMINLTLPKSKGQVQLSGSHKWSYFIKRRRRYSKKTACVLPAP 300

311 ERPSQENHRILPENFGSVRSQSSSKFIPGVTCTFEIKPEENSDVHELVRKSVTRIK 370  
301 ERPSQENHRILPENFGSVRSQSSSKFIPGVTCTFEIKPEENSDVHELVRKSVTRIK 360

371 KRERSVVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIHLLGMSCCL 430  
361 KRERSVVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIHLLGMSCCL 420

431 NPILYGLNNGIKADLVSLIHCLHM 455  
421 NPILYGLNNGIKADLVSLIHCLHM 445

RESULT 12  
US-09-235-839-6  
; Sequence 6, Application US/09235839  
; Patent No. 6207799  
; GENERAL INFORMATION:  
; APPLICANT: Hu Ph.D., Yinghe  
; APPLICANT: McCaleb Ph.D., Michael L.  
; APPLICANT: Bloomquist Ph.D., Brian T.  
; APPLICANT: Flores-Riveros Ph.D., Jaime R.  
; APPLICANT: Cornfield Ph.D., Linda J.  
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/235,839  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/630,118  
; FILING DATE: April 8, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greenfield Ph.D., Michael S.  
; REGISTRATION NUMBER: 37,142  
; REFERENCE/DOCKET NUMBER: 96,149-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)913-0001

TELEFAX: (312)913-0002

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 445 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-235-839-6

Query Match 97.7%; Score 2330; DB 3; Length 445;

Best Local Similarity 100.0%; Pred. No. 1.1e-175;

Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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121 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAICSLPVFHS 180

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241 GLSNKENRLEENEMINLTLPKSKGQVQLSGSHKWSYFIKRRRRYSKKTACVLPAP 300

311 ERPSQENHRILPENFGSVRSQSSSKFIPGVTCTFEIKPEENSDVHELVRKSVTRIK 370

301 ERPSQENHRILPENFGSVRSQSSSKFIPGVTCTFEIKPEENSDVHELVRKSVTRIK 360

371 KRERSVVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIHLLGMSCCL 430

361 KRERSVVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIHLLGMSCCL 420

431 NPILYGLNNGIKADLVSLIHCLHM 455

421 NPILYGLNNGIKADLVSLIHCLHM 445

RESULT 13

US-09-327-035-6

; Sequence 6, Application US/09327035

; Patent No. 6368824

; GENERAL INFORMATION:

; APPLICANT: Hu Ph.D., Yinghe

; APPLICANT: McCaleb Ph.D., Michael L.

; APPLICANT: Bloomquist Ph.D., Brian T.

; APPLICANT: Flores-Riveros Ph.D., Jaime R.

; APPLICANT: Cornfield Ph.D., Linda J.

; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/327,035
; FILING DATE: 07-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,399
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-327-035-6

Query Match          97.7%; Score 2330; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.1e-175;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYNNKTLATENNNTAATRNDFPVDYKSSVDDLOVFLIGLYTFVSLGFMGNL 70
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QY 71 LILMALMKRNQKTTNFIENLAFSDILVLFPCSPFTLTSLVLDQWFMGKVMCHIMPFL 130
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; Sequence 2, Application US/09065027
; Patent No. 6528303
; GENERAL INFORMATION:
; APPLICANT: Heizog, H.
; TITLE OF INVENTION: NEUROPEPTIDE Y-Y5 RECEPTOR
; FILE REFERENCE: 273402001800
; CURRENT APPLICATION NUMBER: US/09/065,027
; CURRENT FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT/AU96/00706
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 8

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/327,035
; FILING DATE: 07-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,399
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-327-035-6

Query Match          97.7%; Score 2330; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.1e-175;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 371 KRSRSVFRLTILILVFAVSNMPLHFLHVVTDFNDNLISNRHFKLVYICILLGMSCCL 430
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; Sequence 13, Application US/09708392
; Patent No. 6734186
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc
; APPLICANT: Pfizer Limited
; APPLICANT: Wayman, Chris
; APPLICANT: Naw, G
; TITLE OF INVENTION: Pharmaceutical
; FILE REFERENCE: PC10343AAKM
; CURRENT APPLICATION NUMBER: US/09/708,392
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: GB 99266437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
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; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/221,093
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; TYPE: PRT
; LENGTH: 445
; ORGANISM: Homo sapiens
; US-09-708-392-13

Query Match 97.7%; Score 2330; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.le-175; Indels 0; Gaps 0;
Matches 445; Conservative 0; Mismatches 0;

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Search completed: October 21, 2004, 12:14:48
Job time : 40 secs



GenCore version 5.1.6  
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 12:07:45 ; Search time 129 Seconds  
(without alignments)  
1141.939 Million cell updates/sec

Title: US-09-771-956-13

Perfect score: 2385

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 1          | 2385   | 100.0       | 455    | US-09-771-956-13   | Sequence 13, Appli |
| 2          | 2385   | 100.0       | 455    | US-09-771-956-13   | Sequence 4, Appli  |
| 3          | 2385   | 100.0       | 455    | US-09-771-956-13   | Sequence 7, Appli  |
| 4          | 2385   | 100.0       | 455    | US-09-771-956-13   | Sequence 7, Appli  |
| 5          | 2373   | 99.5        | 455    | US-09-771-956-13   | Sequence 30, Appli |
| 6          | 2368   | 99.3        | 455    | US-09-771-956-13   | Sequence 7, Appli  |
| 7          | 2330   | 97.7        | 445    | US-10-027-049-2    | Sequence 6, Appli  |
| 8          | 2330   | 97.7        | 445    | US-10-027-049-2    | Sequence 205, App  |
| 9          | 2330   | 97.7        | 445    | US-10-225-567A-205 | Sequence 668, App  |
| 10         | 2330   | 97.7        | 445    | US-10-225-567A-205 | Sequence 14, Appli |
| 11         | 2326   | 97.5        | 445    | US-10-181-906-9    | Sequence 9, Appli  |
| 12         | 2321   | 97.3        | 445    | US-09-771-956-9    | Sequence 533, App  |
| 13         | 2084.5 | 87.4        | 456    | US-09-826-509-533  | Sequence 2, Appli  |
| 14         | 2074.5 | 87.0        | 445    | US-10-027-049-4    | Sequence 4, Appli  |

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| 15 | 2067.5 | 86.7 | 445 | 14 | US-10-027-049-2    | Sequence 2, Appli  |
| 16 | 2030.5 | 85.1 | 499 | 9  | US-09-771-956-24   | Sequence 24, Appli |
| 17 | 2017   | 84.6 | 508 | 9  | US-09-771-956-22   | Sequence 22, Appli |
| 18 | 1671   | 70.1 | 334 | 9  | US-09-963-646-6    | Sequence 6, Appli  |
| 19 | 1668.5 | 70.0 | 350 | 9  | US-09-771-956-6    | Sequence 6, Appli  |
| 20 | 1609.5 | 67.5 | 394 | 9  | US-09-771-956-10   | Sequence 10, Appli |
| 21 | 1609.5 | 67.5 | 394 | 14 | US-10-013-846-17   | Sequence 17, Appli |
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| 23 | 1587.5 | 66.6 | 394 | 14 | US-10-274-851-17   | Sequence 17, Appli |
| 24 | 1575.5 | 66.1 | 341 | 9  | US-09-771-956-20   | Sequence 20, Appli |
| 25 | 1533.5 | 64.3 | 352 | 9  | US-09-771-956-23   | Sequence 23, Appli |
| 26 | 1531.5 | 64.2 | 341 | 9  | US-09-771-956-26   | Sequence 26, Appli |
| 27 | 1525.5 | 64.0 | 383 | 9  | US-09-771-956-21   | Sequence 21, Appli |
| 28 | 1479.5 | 62.0 | 383 | 9  | US-09-771-956-27   | Sequence 27, Appli |
| 29 | 1479.5 | 62.0 | 395 | 9  | US-09-771-956-25   | Sequence 25, Appli |
| 30 | 497    | 20.8 | 371 | 14 | US-10-081-810-49   | Sequence 49, Appli |
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| 33 | 481.5  | 20.2 | 384 | 14 | US-10-013-846-4    | Sequence 4, Appli  |
| 34 | 481.5  | 20.2 | 384 | 14 | US-10-176-847-26   | Sequence 26, Appli |
| 35 | 481.5  | 20.2 | 384 | 14 | US-10-225-567A-378 | Sequence 378, App  |
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| 39 | 481.5  | 20.2 | 384 | 14 | US-10-291-390-31   | Sequence 31, Appli |
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| 41 | 481.5  | 20.2 | 384 | 14 | US-10-295-027-640  | Sequence 640, App  |
| 42 | 481.5  | 20.2 | 384 | 14 | US-10-295-027-746  | Sequence 746, App  |
| 43 | 481.5  | 20.2 | 384 | 15 | US-10-410-648-4    | Sequence 4, Appli  |
| 44 | 481.5  | 20.2 | 388 | 15 | US-10-181-906-6    | Sequence 6, Appli  |
| 45 | 481.5  | 20.2 | 383 | 14 | US-10-081-810-50   | Sequence 50, Appli |

## ALIGNMENTS

RESULT 1  
US-09-771-956-13  
; Sequence 13, Application US/09771956  
; Patent No. US20010031474A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Michele  
; APPLICANT: Brodebeck, Robbin  
; APPLICANT: Krause, James  
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
; FILE REFERENCE: N2000.001  
; CURRENT APPLICATION NUMBER: US/09/771,956  
; CURRENT FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-956-13

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| Best Local Similarity | 100.0%; | Pred. No.  | 1e-191; |            |    |        |      |
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RESULT 2  
US-09-962-646-4  
; Sequence 4, Application US/09962646  
; Patent No. US20020103123A1  
; GENERAL INFORMATION:  
; APPLICANT: GERALD, CHRISTOPHE P.G.  
; APPLICANT: WEINSHANK, RICHARD L.  
; APPLICANT: WALKER, MARY W  
; APPLICANT: BRANCHEK, THERESA  
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND  
; TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR  
; FILE REFERENCE: 1795/461668ZA  
; CURRENT APPLICATION NUMBER: US/09/962,646  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/200,673  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: 08/566,096  
; PRIOR FILING DATE: 1995-12-01  
; PRIOR APPLICATION NUMBER: 08/349,025  
; PRIOR FILING DATE: 1994-12-01  
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; SOFTWARE: PatentIn version 3.1  
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; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-962-646-4

Query Match 100.0%; Score 2385; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1e-191;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDYNNKTLATENNNTAATRNSDPFWDDYKSDVDDLOQYFLIGLYTF 60  
Db 1 MSFYSKQDYNMDELDYNNKTLATENNNTAATRNSDPFWDDYKSDVDDLOQYFLIGLYTF 60  
QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWFG 120  
Db 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWFG 120  
QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVTLGFAI 180  
Db 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVTLGFAI 180  
QY 181 CSPLPVHSLVLOETFGSALLSSRLVCSWPSDSYRIAFITSLLLVQYILPLVCLTVS 240  
Db 181 CSPLPVHSLVLOETFGSALLSSRLVCSWPSDSYRIAFITSLLLVQYILPLVCLTVS 240  
QY 241 HTSVCRSISCGLSKNENRLEENEMINLTLPKSKGPGQVLSGSHKWSYFPIKGRHRRYS 300  
Db 241 HTSVCRSISCGLSKNENRLEENEMINLTLPKSKGPGQVLSGSHKWSYFPIKGRHRRYS 300  
QY 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPCTCFEIKPEENSVDVHEL 360  
Db 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPCTCFEIKPEENSVDVHEL 360  
QY 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420

Db 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPCTCFEIKPEENSVDVHEL 360  
QY 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
QY 421 HLLGMSCCLNPILYGFLLNGIKADLVSLIHCLHM 455  
Db 421 HLLGMSCCLNPILYGFLLNGIKADLVSLIHCLHM 455

RESULT 3  
US-10-013-846-7  
; Sequence 7, Application US/10013846  
; Publication No. US20030036652A1  
; GENERAL INFORMATION:  
; APPLICANT: Baktavatchalam, Rajagopal  
; APPLICANT: Blum, Charles A  
; APPLICANT: Darrow, James W  
; APPLICANT: De Lombaert, Stephane  
; APPLICANT: Hutchison, Alan  
; APPLICANT: Tran, Jennifer  
; APPLICANT: Zheng, Xiaozhang  
; APPLICANT: Elliott, Richard L  
; APPLICANT: Hammond, Marlys  
; TITLE OF INVENTION: Spiro[sobenzofuran-1,4'-piperidin]-3-ones and  
; TITLE OF INVENTION: 3H-spiro[sobenzofuran-1,4'-piperidines  
; FILE REFERENCE: N00.2001  
; CURRENT APPLICATION NUMBER: US/10/013,846  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 60/254,990  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: homosapiens  
US-10-013-846-7

Query Match 100.0%; Score 2385; DB 14; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1e-191;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDYNNKTLATENNNTAATRNSDPFWDDYKSDVDDLOQYFLIGLYTF 60  
Db 1 MSFYSKQDYNMDELDYNNKTLATENNNTAATRNSDPFWDDYKSDVDDLOQYFLIGLYTF 60  
QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWFG 120  
Db 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWFG 120  
QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVTLGFAI 180  
Db 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVTLGFAI 180  
QY 181 CSPLPVHSLVLOETFGSALLSSRLVCSWPSDSYRIAFITSLLLVQYILPLVCLTVS 240  
Db 181 CSPLPVHSLVLOETFGSALLSSRLVCSWPSDSYRIAFITSLLLVQYILPLVCLTVS 240  
QY 241 HTSVCRSISCGLSKNENRLEENEMINLTLPKSKGPGQVLSGSHKWSYFPIKGRHRRYS 300  
Db 241 HTSVCRSISCGLSKNENRLEENEMINLTLPKSKGPGQVLSGSHKWSYFPIKGRHRRYS 300  
QY 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPCTCFEIKPEENSVDVHEL 360  
Db 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPCTCFEIKPEENSVDVHEL 360  
QY 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420



QY 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455  
Db 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455

## RESULT 4

US-10-410-648-7  
; Sequence 7, Application US/10410648  
; Publication No. US20040072847A1  
; GENERAL INFORMATION:  
; APPLICANT: Bakthavatchalam, Rajagopal  
; APPLICANT: Blum, Charles A.  
; APPLICANT: Brielmann, Harry L.  
; APPLICANT: Darrow, James W.  
; APPLICANT: De Lombaert, Stephanie W.  
; APPLICANT: Hutchinson, Alan W.  
; APPLICANT: Tran, Jennifer W.  
; APPLICANT: Zheng, Xiaozhang W.  
; APPLICANT: Elliott, Richard L.  
; APPLICANT: Hammond, Marlys L.  
; TITLE OF INVENTION: SPIROISOBOFURAN-1,4'-PIPERIDIN-3-ONES AND  
; FILE REFERENCE: U 014539-7  
; CURRENT APPLICATION NUMBER: US/10/410,648  
; PRIOR FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: 10/013,846  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: 60/254,990  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 7  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-410-648-7

Query Match 100.0%; Score 2385; DB 15; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1e-191;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSFYSKQDYNMDELDYVYKTLATENTATRNSDFFVWDYKSSVDDLOQYFLIGLYTF 60  
Db 1 MSFYSKQDYNMDELDYVYKTLATENTATRNSDFFVWDYKSSVDDLOQYFLIGLYTF 60  
QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120  
Db 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120  
QY 121 KVMCHIMPLOQVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVMTLGF 180  
Db 121 KVMCHIMPLOQVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVMTLGF 180  
QY 181 CSPLPVFHSLVLOETFGSALLSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240  
Db 181 CSPLPVFHSLVLOETFGSALLSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240  
QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKHHRRYS 300  
Db 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKHHRRYS 300  
QY 301 KKTACVLPAPERPSQENHSRIIPENFGSVRSQSSSKFIPGVPTCTPEIKPEENS DVHEL 360  
Db 301 KKTACVLPAPERPSQENHSRIIPENFGSVRSQSSSKFIPGVPTCTPEIKPEENS DVHEL 360  
QY 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPHLHFHVWTFDNDNLISNRHFKLVYCIC 420  
Db 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPHLHFHVWTFDNDNLISNRHFKLVYCIC 420  
QY 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455  
Db 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455

## RESULT 5

US-09-771-956-30  
; Sequence 30, Application US/09771956  
; Patent No. US20010031474A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Michele  
; APPLICANT: Brodbeck, Robbin  
; APPLICANT: Krause, James  
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
; FILE REFERENCE: N2000.001  
; CURRENT APPLICATION NUMBER: US/09/771,956  
; CURRENT FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patent in ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Cercopithecus aethiops  
US-09-771-956-30

Query Match 99.5%; Score 2373; DB 9; Length 455;  
Best Local Similarity 99.3%; Pred. No. 1e-190;  
Matches 452; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSFYSKQDYNMDELDYVYKTLATENTATRNSDFFVWDYKSSVDDLOQYFLIGLYTF 60  
Db 1 MSFYSKQDYNMDELDYVYKTLATENTATRNSDFFVWDYKSSVDDLOQYFLIGLYTF 60  
QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120  
Db 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120  
QY 121 KVMCHIMPLOQVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVMTLGF 180  
Db 121 KVMCHIMPLOQVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVMTLGF 180  
QY 181 CSPLPVFHSLVLOETFGSALLSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240  
Db 181 CSPLPVFHSLVLOETFGSALLSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240  
QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKHHRRYS 300  
Db 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKHHRRYS 300  
QY 301 KKTACVLPAPERPSQENHSRIIPENFGSVRSQSSSKFIPGVPTCTPEIKPEENS DVHEL 360  
Db 301 KKTACVLPAPERPSQENHSRIIPENFGSVRSQSSSKFIPGVPTCTPEIKPEENS DVHEL 360  
QY 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPHLHFHVWTFDNDNLISNRHFKLVYCIC 420  
Db 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPHLHFHVWTFDNDNLISNRHFKLVYCIC 420  
QY 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455  
Db 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455

## RESULT 6

US-10-274-851-7  
; Sequence 7, Application US/10274851  
; Publication No. US20030144290A1  
; GENERAL INFORMATION:  
; APPLICANT: Blum, Charles  
; APPLICANT: Brielmann, Harry  
; APPLICANT: De Lombaert, Stephanie  
; APPLICANT: Zheng, Xiaozhang  
; TITLE OF INVENTION: SUBSTITUTE 2-CYCLOHEXYL-4-PHENYL-1H-IMIDAZOLE  
; FILE REFERENCE: U 014209-8  
; CURRENT APPLICATION NUMBER: US/10/274,851  
; CURRENT FILING DATE: 2002-10-21

NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: Patent in Ver. 2.0  
 SEQ ID NO 7  
 LENGTH: 455  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-274-851-7

Query Match 99.3%; Score 2368; DB 14; Length 455;  
 Best Local Similarity 99.6%; Pred. No. 2.7e-190;  
 Matches 453; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MSFYSKQDYNMDELDYYNKTATENNATARNSDPFWDDYKSSVDDQYFLGLYTF      | 60  |
| DB | 1   | MSFYSKQDYNMDELDYYNKTATENNATARNSDPFWDDYKSSVDDQYFLGLYTF      | 60  |
| QY | 61  | VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG     | 120 |
| DB | 61  | VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG     | 120 |
| QY | 121 | KVMCHMPFQCVSLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVMTLGPFI  | 180 |
| DB | 121 | KVMCHMPFQCVSLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVMTLGPFI  | 180 |
| QY | 181 | CSPLPVFHSVLEQTFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS | 240 |
| DB | 181 | CSPLPVFHSVLEQTFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS | 240 |
| QY | 241 | HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKRRRYS     | 300 |
| DB | 241 | HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKRRRYS     | 300 |
| QY | 301 | KKTACVLPAPEPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDVHEL | 360 |
| DB | 301 | KKTACVLPAPEPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDVHEL | 360 |
| QY | 361 | RVKRSVTRIKRSRVFVRLTILVFAVSWMPLHLFHVTFDNDNLISNRHFKLVYCIC    | 420 |
| DB | 361 | RVKRSVTRIKRSRVFVRLTILVFAVSWMPLHLFHVTFDNDNLISNRHFKLVYCIC    | 420 |
| QY | 421 | HLLGMMSCCLPILYGFNLNGIKADLVSLIHCLHM                         | 455 |
| DB | 421 | HLLGMMSCCLPILYGFNLNGIKADLVSLIHCLHM                         | 455 |

## RESULT 7

US-10-027-049-6  
 Sequence 6, Application US/10027049  
 Publication No. US2003002283A1

## GENERAL INFORMATION:

APPLICANT: Hu Ph.D., Yinghe  
 McCaleb Ph.D., Michael L.  
 Bloomquist Ph.D., Brian T.  
 Flores-Riveros Ph.D., Jaime R.  
 Cornfield Ph.D., Linda J.  
 TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid Sequences

## NUMBER OF SEQUENCES: 8

## CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
 STREET: 300 South Wacker Drive, 32nd Floor  
 CITY: Chicago  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/027,049  
 FILING DATE: 08-Apr-1996

## CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:  
 NAME: Greenfield Ph.D., Michael S.  
 REGISTRATION NUMBER: 37,142  
 REFERENCE/DOCKET NUMBER: 96,149/WH 405  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 715-1000  
 TELEFAX: (312) 715-1234

## INFORMATION FOR SEQ ID NO: 6:

## SEQUENCE CHARACTERISTICS:

LENGTH: 445 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-027-049-6

Query Match 97.7%; Score 2330; DB 14; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-187;  
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 11  | MDLEDEYNNKTLATENNATARNSDPFWDDYKSSVDDQYFLGLYTFVSLGFMGNL       | 70  |
| DB | 1   | MDLEDEYNNKTLATENNATARNSDPFWDDYKSSVDDQYFLGLYTFVSLGFMGNL       | 60  |
| QY | 71  | LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFGKVMCHMPFL       | 130 |
| DB | 61  | LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFGKVMCHMPFL       | 120 |
| QY | 131 | QCYSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVMTLGPFI           | 190 |
| DB | 121 | QCYSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVMTLGPFI           | 180 |
| QY | 191 | VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC | 250 |
| DB | 181 | VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC | 240 |
| QY | 251 | GLSNKENRLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKRRRYSKKTACVLPA       | 310 |
| DB | 241 | GLSNKENRLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKRRRYSKKTACVLPA       | 300 |
| QY | 311 | ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDVHELVRKSVTRIK   | 370 |
| DB | 301 | ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDVHELVRKSVTRIK   | 360 |
| QY | 371 | KRSRSVFVRLTILVFAVSWMPLHLFHVTFDNDNLISNRHFKLVYCICHLGMMSCCL     | 430 |
| DB | 361 | KRSRSVFVRLTILVFAVSWMPLHLFHVTFDNDNLISNRHFKLVYCICHLGMMSCCL     | 420 |
| QY | 431 | NFILYGFNLNGIKADLVSLIHCLHM                                    | 455 |
| DB | 421 | NFILYGFNLNGIKADLVSLIHCLHM                                    | 445 |

## RESULT 8

US-10-225-567A-205  
 Sequence 205, Application US/10225567A  
 Publication No. US20030113798A1

## GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences  
 APPLICANT: Brown, Joseph P.  
 APPLICANT: Burner, Glenna C.  
 APPLICANT: Roush, Christine L.  
 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 FILE REFERENCE: 1920-4-4  
 CURRENT APPLICATION NUMBER: US/10/225,567A  
 CURRENT FILING DATE: 2001-12-19  
 PRIOR APPLICATION NUMBER: 60/257,144  
 PRIOR FILING DATE: 2000-12-19  
 NUMBER OF SEQ ID NOS: 2292  
 SOFTWARE: Patent in version 3.1  
 SEQ ID NO 205  
 LENGTH: 445

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-205

Query Match
Best Local Similarity 97.7%; Score 2330; DB 14; Length 445;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MDLEDEYNNKTATENNNTAATNSDPVWDDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 70
Db 1 MDLEDEYNNKTATENNNTAATNSDPVWDDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 60

Qy 71 LILMALMKKNQKTTNVFNIGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHIMPF 130
Db 61 LILMALMKKNQKTTNVFNIGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHIMPF 120

Qy 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGFIATWTLGFAICSPPLVFHSL 190
Db 121 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGFIATWTLGFAICSPPLVFHSL 180

Qy 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 250
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 240

Qy 251 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 310
Db 241 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 300

Qy 311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELAVKRSVTRIK 370
Db 301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELAVKRSVTRIK 360

Qy 371 KRRSVYFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 430
Db 361 KRRSVYFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 420

Qy 431 NPILYGLFNGIKADLVSLIHCLHM 455
Db 421 NPILYGLFNGIKADLVSLIHCLHM 445
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## RESULT 9

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US-10-295-027-668
; Sequence 668, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
```

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; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 668
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-668
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Query Match 97.7%; Score 2330; DB 14; Length 445;

Best Local Similarity 100.0%; Pred. No. 4.1e-187;

Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 11 MDLEDEYNNKTATENNNTAATNSDPVWDDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 70
Db 1 MDLEDEYNNKTATENNNTAATNSDPVWDDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 60

Qy 71 LILMALMKKNQKTTNVFNIGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHIMPF 130
Db 61 LILMALMKKNQKTTNVFNIGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHIMPF 120

Qy 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGFIATWTLGFAICSPPLVFHSL 190
Db 121 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGFIATWTLGFAICSPPLVFHSL 180

Qy 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 250
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 240

Qy 251 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 310
Db 241 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 300

Qy 311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELAVKRSVTRIK 370
Db 301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELAVKRSVTRIK 360

Qy 371 KRRSVYFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 430
Db 361 KRRSVYFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 420

Qy 431 NPILYGLFNGIKADLVSLIHCLHM 455
Db 421 NPILYGLFNGIKADLVSLIHCLHM 445
```

## RESULT 10

```
US-10-181-906-14
; Sequence 14, Application US/10181906
; Publication No. US20040053864A1
; GENERAL INFORMATION:
; APPLICANT: Karsenty, Gerard
; APPLICANT: Amling, Michael
; APPLICANT: Ducey, Patricia
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA
; TITLE OF INVENTION: MODULATION OF NEUROPEPTIDE Y ACTIVITY
; FILE REFERENCE: 9142-020-999
; CURRENT APPLICATION NUMBER: US/10/181,906
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/02040
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 445
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-181-906-14

Query Match 97.7%; Score 2330; DB 15; Length 445;  
Best Local Similarity 100.0%; Pred. No. 4.1e-187;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYKNTLATENNTAATNSDPVWDDYKSSVDDLOQYFLIGLTYFVSLIGFMGNL 70  
DB 1 MDLEDEYKNTLATENNTAATNSDPVWDDYKSSVDDLOQYFLIGLTYFVSLIGFMGNL 60  
QY 71 LILMALKRKNQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHMPFL 130  
DB 61 LILMALKRKNQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHMPFL 120  
QY 131 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHYFLIATVTLGFAICSPLPVHSL 190  
DB 121 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHYFLIATVTLGFAICSPLPVHSL 180  
QY 191 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 250  
DB 181 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 240  
QY 251 GLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 310  
DB 241 GLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 300  
QY 311 ERPSQENSHRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHSLRVKRSVTRIK 370  
DB 301 ERPSQENSHRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHSLRVKRSVTRIK 360  
QY 371 KRSRSVFRLTLLILVFAVSWMPLHLFHVVTDFDNLISNRHFKLVYICHLIGMWSCLL 430  
DB 361 KRSRSVFRLTLLILVFAVSWMPLHLFHVVTDFDNLISNRHFKLVYICHLIGMWSCLL 420  
QY 431 NPILYGLNNGIKADLVSLIHLCHM 455  
DB 421 NPILYGLNNGIKADLVSLIHLCHM 445

## RESULT 11

US-09-771-956-9  
; Sequence 9, Application US/09771956  
; Patent No. US20010031474A1

; GENERAL INFORMATION:  
; APPLICANT: Bennett, Michele  
; APPLICANT: Brodebeck, Robbin  
; APPLICANT: Krause, James  
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
; FILE REFERENCE: N2000.001  
; CURRENT APPLICATION NUMBER: US/09/771,956  
; CURRENT FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Y5/Y1 CHIMERA

US-09-771-956-9

Query Match 97.5%; Score 2326; DB 9; Length 499;  
Best Local Similarity 99.6%; Pred. No. 1e-186;  
Matches 444; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDLEDEYKNTLATENNTAATNSDPVWDDYKSSVDDLOQYFLIGLTYF 60  
DB 1 MSFYSKQDYNMDLEDEYKNTLATENNTAATNSDPVWDDYKSSVDDLOQYFLIGLTYF 60  
QY 61 VSLIGFMGNLILMALMKRKNQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120

DB 61 VSLIGFMGNLILMALMKRKNQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120  
QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHYFLIATVTLGFAI 180  
DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHYFLIATVTLGFAI 180  
QY 181 CSPLPVHSLVELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240  
DB 181 CSPLPVHSLVELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240  
QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYS 300  
DB 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYS 300  
QY 301 KKTACVLPAPERPSQENSHRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHSL 360  
DB 301 KKTACVLPAPERPSQENSHRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHSL 360  
QY 361 RVKRSVTRIKRRSVFRLTLLILVFAVSWMPLHLFHVVTDFDNLISNRHFKLVYIC 420  
DB 361 RVKRSVTRIKRRSVFRLTLLILVFAVSWMPLHLFHVVTDFDNLISNRHFKLVYIC 420  
QY 421 HLLGMWSCLLNPILYGLNNGIKADL 446  
DB 421 HLLGMWSCLLNPILYGLNNGIKADL 446

## RESULT 12

US-09-826-509-533  
; Sequence 533, Application US/09826509  
; Publication No. US20030204073A1

; GENERAL INFORMATION:  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G  
; FILE REFERENCE: AREN-207  
; CURRENT APPLICATION NUMBER: US/09/826,509  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/195,747  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 589  
; SOFTWARE: Patent in Version 2.1  
; SEQ ID NO 533  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-826-509-533

Query Match 97.3%; Score 2321; DB 10; Length 445;  
Best Local Similarity 99.8%; Pred. No. 2.3e-186;  
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MDLEDEYKNTLATENNTAATNSDPVWDDYKSSVDDLOQYFLIGLTYFVSLIGFMGNL 70  
DB 1 MDLEDEYKNTLATENNTAATNSDPVWDDYKSSVDDLOQYFLIGLTYFVSLIGFMGNL 60  
QY 71 LILMALKRKNQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHMPFL 130  
DB 61 LILMALKRKNQKTTNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHMPFL 120  
QY 131 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHYFLIATVTLGFAICSPLPVHSL 190  
DB 121 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHYFLIATVTLGFAICSPLPVHSL 180  
QY 191 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 250  
DB 181 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 240  
QY 251 GLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 310

Db 241 GLSNKENRLEENEMINLTLPKSKQPOVKLSGSHKWSYFPIKHRRYSKKTACVLPAP 300  
QY 311 ERPSQNHRRILPENFGSVRSQSSSKFIPGVPCTCFIKPEENSDVHRLVKSVTRIK 370  
Db 301 ERPSQNHRRILPENFGSVRSQSSSKFIPGVPCTCFIKPEENSDVHRLVKSVTRIK 360  
QY 371 KGRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIHLLGMSCCL 430  
Db 361 KGRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIHLLGMSCCL 420  
QY 431 NPILYGLFNGIKADLVSLIHCLHM 455  
Db 421 NPILYGLFNGIKADLVSLIHCLHM 445

RESULT 13  
US-09-962-646-2  
; Sequence 2, Application US/09962646  
; Patent No. US20020103123A1  
; GENERAL INFORMATION:  
; APPLICANT: GERALD, CHRISTOPHE P.G.  
; APPLICANT: WEINSHANK, RICHARD L.  
; APPLICANT: WALKER, MARY W  
; APPLICANT: BRANCHER, THERESA  
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND  
; TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE V/PEPTIDE YY RECEP  
; FILE REFERENCE: 1795/461682A  
; CURRENT APPLICATION NUMBER: US/09/962,646  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/200,673  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: 08/566,096  
; PRIOR FILING DATE: 1995-12-01  
; PRIOR APPLICATION NUMBER: 08/349,025  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; TYPE: PRT  
; LENGTH: 456  
; ORGANISM: Rattus No. US20020103123A1vegicus  
US-09-962-646-2

Query Match 87.4%; Score 2084.5; DB 9; Length 456;  
Best Local Similarity 88.2%; Pred. No. 1.8e-166;  
Matches 396; Conservative 22; Mismatches 30; Indels 1; Gaps 1;

QY 7 QDYNMDELDEYNNKTATENNNTAATRNSDPFVMDYKSSVDDLYQYFLIGLYTFVSLIGF 66  
Db 8 QDSSMEFKLEEHNKFTVTENNTAARNAAPAWEDYRGSVDDLYQYFLIGLYTFVSLIGF 67

QY 67 MGNLLILMALMKRQKQTTWNFLGNLAFSDILVLFCSPTLTSVLLDQWFMGKWMCHI 126  
Db 68 MGNLLILMALMKRQKQTTWNFLGNLAFSDILVLFCSPTLTSVLLDQWFMGKWMCHI 127

QY 127 MPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGFALCSPLPV 186  
Db 128 MPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGFALCSPLPV 187

QY 187 FHSVLQTFGSALLSSRYLCVSWPDSYRIAPTISLLLVQVILPVCLTVSHTSVCR 246  
Db 188 FHSVLQTFGSALLSSRYLCVSWPDSYRIAPTISLLLVQVILPVCLTVSHTSVCR 247

QY 247 SISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFPIKHRRYSKKTACV 306  
Db 248 SISCGLSHKNLEENEMINLTLPKSKSRNOAKTPTCKWSYFIRKGRYRSKKTACV 307

QY 307 LPAPERPSQENSRILPENFGSVRSQSSSKFIPGVPCTCFIKPEENSDVHRLVKRSV 366  
Db 308 LPAPERPSQENSRILPENFGSVRSQSSSKFIPGVPCTCFIKPEENSDVHRLVKRSV 366

QY 367 TRIKRSRSVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIHLLGM 426

Db 367 TRIKRSRSVFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIHLLGM 426  
QY 427 SCCLNPILYGLFNGIKADLVSLIHCLHM 455  
Db 427 SCCLNPILYGLFNGIKADLVSLIHCLHM 455

RESULT 14  
US-10-027-049-4  
; Sequence 4, Application US/10027049  
; Publication No. US2003002283A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu Ph.D., Yinghe  
; McCaleb Ph.D., Michael L.  
; Bloomquist Ph.D., Brian T.  
; Flores-Riveros Ph.D., Jaime R.  
; Cornfield Ph.D., Linda J.  
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive, 32nd Floor  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/027,049  
; FILING DATE: 08-Apr-1996  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greentield Ph.D., Michael S.  
; REGISTRATION NUMBER: 37,142  
; REFERENCE/DOCKET NUMBER: 96,149/WH 405  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)715-1000  
; TELEFAX: (312)715-1234  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-027-049-4

Query Match 87.0%; Score 2074.5; DB 14; Length 445;  
Best Local Similarity 88.5%; Pred. No. 1.2e-165;  
Matches 394; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

QY 11 MDELDEYNNKTATENNNTAATRNSDPFVMDYKSSVDDLYQYFLIGLYTFVSLIGF 70  
Db 1 MEFKLEEHNFNTVTENNTAARNAAPAWEDYRGSVDDLYQYFLIGLYTFVSLIGF 60

QY 71 LILMALMKRQKQTTWNFLGNLAFSDILVLFCSPTLTSVLLDQWFMGKWMCHI 130  
Db 61 LILMALMKRQKQTTWNFLGNLAFSDILVLFCSPTLTSVLLDQWFMGKWMCHI 120

QY 131 QCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGFALCSPLPVFHS 190  
Db 121 QCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGFALCSPLPVFHS 180

QY 191 VELQTFGSALLSSRYLCVSWPDSYRIAPTISLLLVQVILPVCLTVSHTSVCRSIS 250  
Db 181 VELQTFGSALLSSRYLCVSWPDSYRIAPTISLLLVQVILPVCLTVSHTSVCRSIS 240

QY 251 GLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 310  
 Db 241 GLSHKENRLEENEMINLTLPKSKSRNOAKTPSTQKWSYFIRKRRYSKKTACVLPAP 300  
 QY 311 ERPSQENHRIIPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKRSVTRIK 370  
 Db 301 AGPSQCKHLAV-PENPASVRSQSSSKVPGVPICFEVKPESSDAHEMRVRSITRIK 359  
 QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 430  
 Db 360 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 419  
 QY 431 NPILYGLFNNGIKADLVSLIHCLHM 455  
 Db 420 NPILYGLFNNGIKADLVSLIHCLHM 444

## RESULT 15

US-10-027-049-2

; Sequence 2, Application US/10027049

; Publication No. US2003002283A1

; GENERAL INFORMATION:

; APPLICANT: Hu Ph.D., Yinghe

; McCaleb Ph.D., Michael L.

; Bloomquist Ph.D., Brian T.

; Flores-Riveros Ph.D., Jaime R.

; Cornfield Ph.D., Linda J.

; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

; Sequences

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert &amp; Berghoff

; STREET: 300 South Wacker Drive, 32nd Floor

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/027,049

; FILING DATE: 08-Apr-1996

; CLASSIFICATION: &lt;unknown&gt;

; ATTORNEY/AGENT INFORMATION:

; NAME: Greenfield Ph.D., Michael S.

; REGISTRATION NUMBER: 37,142

; REFERENCE/DOCKET NUMBER: 96,149/WH 405

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312)715-1000

; TELEFAX: (312)715-1234

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 445 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-027-049-2

Query Match

Best Local Similarity 86.7%; Score 2067.5; DB 14; Length 445;

Matches 393; Conservative 21; Mismatches 30; Indels 1; Gaps 1;

QY 11 MDLEDEYNNKTLATENNATRNSDFFVWDDYKSSVDDIQYELIGLYTFVSLGFMGNL 70  
 Db 1 MEFKLEHFNKTFVTENTAAARNAAPPAWEDYRGSDVDDQYELIGLYTFVSLGFMGNL 60  
 QY 71 LILMALMKKNQKNTVNFNLGNLAFSDILVLFCSPTLTSLVLLDQWFGKVMCHIMPFL 130  
 Db 61 FILMAYMKKNQKNTVNFNLGNLAFSDILVLFCSPTLTSLVLLDQWFGKVMCHIMPFL 120

QY 131 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYELIATVMTLGFALCSPLPVFHS 190  
 Db 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYELIATVMTLGFALCSPLPVFHS 180  
 QY 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLLVQYILPLVCLTVSHTSVCRSISC 250  
 Db 181 VELKETFGSALLSSRYLCVESWPSDSYRIAFITISLLLVQYILPLVCLTVSHTSVCRSISC 240  
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPAP 310  
 Db 241 GLSHKENRLEENEMINLTLPKSKSRNOAKTPSTQKWSYFIRKRRYSKKTACVLPAP 300  
 QY 311 ERPSQENHRIIPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKRSVTRIK 370  
 Db 301 AGPSQCKHLAV-PENPASVRSQSSSKVPGVPICFEVKPESSDAHEMRVRSITRIK 359  
 QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 430  
 Db 360 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 419  
 QY 431 NPILYGLFNNGIKADLVSLIHCLHM 455  
 Db 420 NPILYGLFNNGIKADLVSLIHCLHM 444

Search completed: October 21, 2004, 12:17:03  
 Job time : 130 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 21, 2004, 11:29:39 ; Search time 205 Seconds

(without alignments)  
4920.716 Million cell updates/sec

Title: US-09-771-956-4

Perfect score: 2480

Sequence: 1 ttttggtctgacaaatgt.....attctcaactgtttaccaagg 1406

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-DB=A\_Geneseq\_23Sep04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771956@cgn 1 1 224 @runat 21102004 103736 9367 -NCPU=6 -ICPU=3  
-NO.WMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_23Sep04: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description        |
|------------|-------|-------------|--------|------------|--------------------|
| 1          | 2385  | 96.2        | 455    | 2 AAR95939 | Aar95939 Human Y5  |
| 2          | 2385  | 96.2        | 455    | 2 AAW29447 | Aaw29447 Human hip |
| 3          | 2385  | 96.2        | 455    | 2 AAW29413 | Aaw29413 Human hip |
| 4          | 2385  | 96.2        | 455    | 2 AAW37093 | Aaw37093 Homo sapi |
| 5          | 2385  | 96.2        | 455    | 2 AAY57461 | Aay57461 Human hip |
| 6          | 2385  | 96.2        | 455    | 4 AAE08002 | Aae08002 Human neu |
| 7          | 2385  | 96.2        | 455    | 5 ABB84497 | Abb84497 Human hip |
| 8          | 2385  | 96.2        | 455    | 5 ABB79510 | Abb79510 Human neu |
| 9          | 2385  | 96.2        | 455    | 5 ABO23266 | Abo23266 Human neu |
| 10         | 2385  | 96.2        | 455    | 8 ADO29564 | Ado29564 Human GPC |

|    |        |      |     |            |                    |
|----|--------|------|-----|------------|--------------------|
| 11 | 2373   | 95.7 | 455 | 4 AAE08016 | Aae08016 African g |
| 12 | 2330   | 94.0 | 445 | 2 AAW27604 | Aaw27604 Human neu |
| 13 | 2330   | 94.0 | 445 | 2 AAW15230 | Aaw15230 Human neu |
| 14 | 2330   | 94.0 | 445 | 2 AAY14554 | Aay14554 Human neu |
| 15 | 2330   | 94.0 | 445 | 3 AAY52578 | Aay52578 Human NPY |
| 16 | 2330   | 94.0 | 445 | 4 AAE07958 | Aae07958 Human neu |
| 17 | 2330   | 94.0 | 445 | 4 AAE06692 | Aae06692 Human neu |
| 18 | 2330   | 94.0 | 445 | 4 AAE07922 | Aae07922 Human neu |
| 19 | 2330   | 94.0 | 445 | 4 AAB85121 | Aab85121 Human neu |
| 20 | 2330   | 94.0 | 445 | 4 AAB85110 | Aab85110 Human neu |
| 21 | 2330   | 94.0 | 445 | 6 ABB81860 | Abb81860 Human neu |
| 22 | 2330   | 94.0 | 445 | 7 ADN39350 | Adn39350 Cancer/an |
| 23 | 2326   | 93.8 | 499 | 4 AAE08004 | Aae08004 Human chi |
| 24 | 2326   | 93.8 | 499 | 5 ABB32254 | Abb32254 Neuropst  |
| 25 | 2321   | 93.6 | 445 | 4 ABB56370 | Abb56370 Non-endog |
| 26 | 2318   | 93.5 | 445 | 4 AAE02851 | Aae02851 Rhesus ne |
| 27 | 2266   | 91.4 | 445 | 3 AAY52577 | Aay52577 Chimeric  |
| 28 | 2362   | 91.2 | 456 | 2 AAW37095 | Aaw37095 Canis dom |
| 29 | 2084.5 | 84.1 | 456 | 2 AAR95940 | Aar95940 Rat Y5 re |
| 30 | 2084.5 | 84.1 | 456 | 2 AAW29446 | Aaw29446 Rat hypot |
| 31 | 2084.5 | 84.1 | 456 | 2 AAW29412 | Aaw29412 Rat hypot |
| 32 | 2084.5 | 84.1 | 456 | 2 AAY37092 | Aay37092 Rattus no |
| 33 | 2084.5 | 84.1 | 456 | 2 ABB84496 | Abb84496 Rat hypot |
| 34 | 2084.5 | 83.6 | 445 | 5 AAW27603 | Aaw27603 Rat neuro |
| 35 | 2074.5 | 83.6 | 445 | 2 AAY14553 | Aay14553 Rat neuro |
| 36 | 2074.5 | 83.6 | 445 | 3 AAY52579 | Aay52579 Rat NPY ( |
| 37 | 2074.5 | 83.6 | 445 | 2 AAW15233 | Aaw15233 Mouse neu |
| 38 | 2074   | 83.6 | 445 | 2 AAW15232 | Aaw15232 Rat neuro |
| 39 | 2072.5 | 83.6 | 445 | 8 ADO29565 | Ado29565 Mouse GPC |
| 40 | 2070   | 83.5 | 466 | 2 AAW27602 | Aaw27602 Rat neuro |
| 41 | 2067.5 | 83.4 | 445 | 2 AAY14552 | Aay14552 Rat neuro |
| 42 | 2067.5 | 83.4 | 445 | 2 AAE08012 | Aae08012 Rat chine |
| 43 | 2030.5 | 81.9 | 499 | 4 AAE08010 | Aae08010 Mouse chi |
| 44 | 2017   | 81.3 | 508 | 4 AAR95941 | Aar95941 Canine Y5 |
| 45 | 1671   | 67.4 | 334 | 2 AAR95941 | Aar95941 Canine Y5 |

## ALIGNMENTS

RESULT 1  
AAR95939  
ID AAR95939 standard; protein; 455 AA.

|    |    |  |                                   |
|----|----|--|-----------------------------------|
| XX | AC | AAR95939;  |                                   |
| XX | DT | 14-OCT-1996 (first entry)  |                                   |
| XX | DE | Human Y5 receptor.   |                                   |
| XX | KW | Y5 receptor; atypical neuropeptide Y1 receptor; feeding behavior;  |                                   |
| KW | KW | G protein-coupled receptor; agonist; antagonist; obesity; bulimia; |                                   |
| KW | KW | anorexia; transgenic animal.                                       |                                   |
| XX | OS | Homo sapiens.  |                                   |
| XX | XX | Key  | Location/Qualifiers               |
| FT | FT | Domain   | 51..77                            |
| FT | FT |  | /label= I                         |
| FT | FT |  | /note= "transmembrane domain I"   |
| FT | FT | Domain   | 88..110                           |
| FT | FT |  | /label= II                        |
| FT | FT |  | /note= "transmembrane domain II"  |
| FT | FT | Domain   | 126..147                          |
| FT | FT |  | /label= III                       |
| FT | FT |  | /note= "transmembrane domain III" |
| FT | FT | Domain   | 166..187                          |
| FT | FT |  | /label= IV                        |
| FT | FT |  | /note= "transmembrane domain IV"  |
| FT | FT | Domain   | 220..242                          |
| FT | FT |  | /label= V                         |
| FT | FT |  | /note= "transmembrane domain V"   |
| FT | FT | Domain   | 380..403                          |
| FT | FT |  | /label= VI                        |





DT 25-MAR-2003 (revised)  
 XX 26-FEB-1998 (first entry)  
 XX Human hippocampal neuropeptide Y Y5 receptor.  
 XX Hippocampal; neuropeptide Y Y5 receptor; NPY Y5; antagonist;  
 KW epileptic seizure; migraine; sleep disturbance; prophylaxis;  
 KW eating disorder; quinzolin-2,4-diazirine.  
 OS Homo sapiens.  
 XX  
 XX W09720822-AL.  
 PN 12-JUN-1997.  
 XX  
 XX 18-NOV-1996; 96WO-EP005066.  
 XX  
 XX 01-DSC-1995; 95US-00566027.  
 XX  
 XX (NOVS ) NOVARTIS AG.  
 XX  
 XX Rueger H, Schmidlin T, Rigollier P, Yamaguchi Y;  
 PI Tintinotblomley M, Schilling W, Criscione L;  
 PI WPI: 1997-319712/29.  
 DR N-PSDB; AA789114.  
 XX  
 XX Use of new and known quinzolin-2,4-diazirine compounds as NPY Y5  
 PT receptor antagonists - for treating and preventing eating disorders,  
 PT diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,  
 PT migraine, sleep disturbance, etc.  
 XX  
 XX Disclosure; Page 127-129; 155pp; English.  
 XX  
 XX The present sequence represents human hippocampal neuropeptide (NP) Y  
 CC receptor subtype Y5, with a pharmacological function associated with for  
 CC example, obesity and eating disorders. The specification relates to a  
 CC method of treatment and prophylaxis of disorders and diseases associated  
 CC with NPY receptor subtype Y5 comprising administering to a warm-  
 CC blooded animal, including man, in need of such treatment a  
 CC therapeutically effective amount of a quinzolin-2,4-diazirine compound.  
 CC These disorders and diseases include e.g. eating disorders, obesity,  
 CC bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss,  
 CC epileptic seizures, migraine, sleep disturbance, pain,  
 CC sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage,  
 CC shock, congestive heart failure, nasal congestion or diarrhoea. (Updated  
 CC on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 455 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1,34e-253 Length: 455  
 Score: 2385.00 Matches: 455  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 96.17% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-771-956-4 (1-1406) x AAW29447 (1-455)  
 Qy 17 ATGCTTTTATCCAGAGGAGCTATATATGATTTAGAGCTCGACGAGTATTATAAC 76  
 Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluAspGluTyrTyrAsn 20  
 Qy 77 AAGACACTTGCACAGAGAATAATCTGCTGCCACTCGGAATCTGATTTCCACTCTGG 136  
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40  
 Qy 137 GATGACTATAAAGCAGCTGTAGATGACTTACAGTATTCTTGTGCTGGCTCTATACATT 196  
 Db 41 AspAspTyrLysSerValAspAspLeuGlnTyrPheLeuLeuGlyLeuTyrThrPhe 60  
 Qy 197 GTAAGCTCTTCTGCTTTATGCGGAATCTACTTATTTTATGCTCTCATGAAAAGCGT 256

|                        |   |   |         |
|------------------------|---|---|---------|
| Db                     | 421   | HisLeuLeuGlyMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn | 444     |
| Qy                     | 1337  | GGGATTAAAGCTGATTAGTGTCCCTTATACACTGCTCTTCATATG             | 1381    |
|                        |   |   |         |
| Db                     | 441   | GlyIleLysAlaAspLeuValSerLeuLeuHisCysLeuHisMet             | 455     |
| RESULT 3               |   |   |         |
| AAW29413               |   |   |         |
| ID                     | AAW29413  | standard; protein; 455 AA.                                |         |
| XX                     | AC  |   |         |
| XX                     | AAW29413;   |   |         |
| XX                     |   |   |         |
| XX                     | 25-MAR-2003   | (revised)   |         |
| DT                     | 24-FEB-1998   | (first entry)   |         |
| XX                     |   |   |         |
| XX                     | Human hippocampal neuropeptide Y Y5 receptor.                             |   |         |
| XX                     |   |   |         |
| KW                     | Human hippocampal neuropeptide Y Y5 receptor; NPV Y5; prophylaxis;        |   |         |
| KW                     | bulimia nervosa; diabetes; dyslipidaemia; hypertension; memory loss;      |   |         |
| KW                     | epileptic seizure; migraine; sleep disturbance; pain; depression;         |   |         |
| KW                     | sexual disorder; anxiety; cerebral haemorrhage, shock; diarrhoea;         |   |         |
| KW                     | congestive heart failure; eating disorder; obesity.                       |   |         |
| XX                     |   |   |         |
| OS                     | Homo sapiens.   |   |         |
| XX                     |   |   |         |
| XX                     | WO9720820-A1.   |   |         |
| XX                     |   |   |         |
| PD                     | 12-JUN-1997.  |   |         |
| XX                     |   |   |         |
| PF                     | 18-NOV-1996;  | 96WO-EP005055.  |         |
| XX                     |   |   |         |
| PR                     | 01-DEC-1995;  | 95US-00566349.  |         |
| XX                     |   |   |         |
| PA                     | (NOVS ) NOVARTIS AG.  |   |         |
| XX                     |   |   |         |
| PI                     | Rueeger H, Schmidlin T, Rigollier P, Yamaguchi Y;                         |   |         |
| PI                     | Tinteinotblomley M, Schilling W, Criscione L;                             |   |         |
| XX                     |   |   |         |
| DR                     | WPI; 1997-319711/29.  |   |         |
| DR                     | N-PSDB; AAT89110.   |   |         |
| XX                     |   |   |         |
| PT                     | Use of new and known hetero:aryl compounds as NPV Y5-receptor antagonists |   |         |
| PT                     | - for treating and preventing eating disorders, diabetes, dyslipidaemia,  |   |         |
| PT                     | hypertension, memory loss, epilepsy, migraine, etc.                       |   |         |
| XX                     |   |   |         |
| PS                     | Disclosure; Page 76-78; 155pp; English.                                   |   |         |
| XX                     |   |   |         |
| CC                     | This sequence represents human hippocampal neuropeptide (NP) Y receptor   |   |         |
| CC                     | subtype Y5, with a pharmacological function associated with for example,  |   |         |
| CC                     | obesity and eating disorders. The specification relates to a method of    |   |         |
| CC                     | treatment and prophylaxis of disorders and diseases associated with       |   |         |
| CC                     | NPY receptor subtype Y5 comprising administering to a warm-blooded        |   |         |
| CC                     | animal, including man, in need of such treatment a therapeutically        |   |         |
| CC                     | effective amount of a new hetero:aryl compound. These disorders and       |   |         |
| CC                     | diseases include e.g. eating disorders, obesity, bulimia nervosa,         |   |         |
| CC                     | diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,   |   |         |
| CC                     | migraine, sleep disturbance, pain, sexual/reproductive disorders,         |   |         |
| CC                     | depression, anxiety, cerebral haemorrhage, shock, congestive heart        |   |         |
| CC                     | failure, nasal congestion or diarrhoea. (Updated on 25-MAR-2003 to        |   |         |
| XX                     | correct.PI field.)  |   |         |
| XX                     |   |   |         |
| SQ                     | Sequence 455 AA;  |   |         |
| Alignment Scores:      |   |   |         |
| Pred. No.:             | 1.34e-253   | Length:   | 455     |
| Score:                 | 2385.00   | Matches:  | 455     |
| Percent Similarity:    | 100.00%   | Conservative:   | 0       |
| Best Local Similarity: | 100.00%   | Mismatches:   | 0       |
| Query Match:           | 96.17%  | Indels:   | 0       |
| DB:                    | 2   | Gaps:   | 0       |
| US-09-771-956-4        | (1-1406) x  | AAW29413  | (1-455) |

```

Db 361 ArgValysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
QY 1157 ACCATACTGATATAGTATTGCTGTAGTGGATGCGCTACACCTTTCCATGGTA 1216
Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
QY 1217 ACTGATTTTAATGACATCTTATTTCAAAATAGGCATTTCAAGTTGGTGTATTCATTGCT 1276
Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
QY 1277 CATTTGTTGGCATGATGCTCTGTCTTAACTCAATTCATATATGGTTTCTTAATAAT 1336
Db 421 HisLeuLeuGlyMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
QY 1337 GCGATTAAAGCTGATTAGTGTCCCTATATACACTGCTTCCATATG 1381
Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

```

RESULT 4  
 AAW37093  
 ID AAW37093 standard; protein; 455 AA.  
 AC AAW37093;  
 DT 08-JUN-1998 (first entry)  
 DE Homo sapiens hippocampal Y5 receptor.  
 XX Hippocampal Y5 receptor; treatment; anorexia; bulimia; obesity;  
 KW feeding behaviour; modification; atypical neuro-peptide.  
 XX Homo sapiens.  
 XX WO9746250-A1.  
 XX 11-DEC-1997.  
 XX 04-JUN-1997; 97WO-US009504.  
 XX 04-JUN-1996; 96US-00668650.  
 XX 21-FEB-1997; 97US-00803600.  
 XX (SYNA-) SYNAPTIC PHARM CORP.  
 XX Gerald CP, Weinshank RL, Walker MW, Branchek T;  
 PI WPT; 1998-051901/05.  
 DR N-PSDB; AAW00622.  
 XX DNA encoding canine hypothalamic atypical neuro-peptide Y/peptide Y5  
 PT receptor, Y5 - useful for identification of compounds which are capable  
 PT of modifying feeding behaviour.  
 XX Disclosure; Fig 6; 273pp; English.

The sequence is that of a hippocampal Y5 receptor (Y5-R). Y5-R can be  
 used in processes to determine whether a chemical compound specifically  
 binds to and activates or inhibits a Y5-R by measuring a second messenger  
 response. The chemical compounds can be used to increase or reduce the  
 activity of a Y5-R. In particular, inhibitors can be used to treat  
 obesity and activators can be used to treat anorexia. Antagonists capable  
 of alleviating (by decreasing the activity of Y5-R) an abnormality can be  
 identified by administering a potential antagonist to a transgenic mammal  
 as above, and determining whether the substance alleviates the physical  
 and behavioural abnormalities displayed by the transgenic mammal as a  
 result of overactivity of a Y5-R. Agonists can be identified in a similar  
 manner, but where the abnormality is alleviated by increasing the  
 activity of Y5-R

XX Sequence 455 AA;  
 SQ

Alignment Scores:

|   |           |   |     |
|---|-----------|---|-----|
| Pred. No.:                                  | 1.34e-253 | Length:   | 455 |
| Score:                                      | 2385.00   | Matches:  | 455 |
| Percent Similarity:                         | 100.00%   | Conservative:   | 0   |
| Best Local Similarity:                      | 100.00%   | Mismatches:   | 0   |
| Query Match:                                | 96.17%    | Indels:   | 0   |
| DB:   | 2         | Gaps:   | 0   |
| US-09-771-956-4 (1-1406) x AAW37093 (1-455) |           |   |     |
| QY  | 17        | ATGTCCTTTTATTTCAAGCAGGACTATAATATGATTAGAGCTCGAGCAGTATTATTAAC   | 76  |
| Db  | 1         | MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn  | 20  |
| QY  | 77        | AAGACACTGGCAGAGAAATACTCTGCTGCCACTCGGAATTTCTGATTCCGAGTCGG      | 136 |
| Db  | 21        | LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp  | 40  |
| QY  | 137       | GATGACTATAAAGCAGTGTAGATGACATTACAGTATTCTTCTGATTGGGCTCTATACATT  | 196 |
| Db  | 41        | AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe  | 60  |
| QY  | 197       | GTAAGTCTTCTTGGCTTTATGGGAATCTACTATTATTTAATGGCTCTCATGAAAAGGT    | 256 |
| Db  | 61        | ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg  | 80  |
| QY  | 257       | AATCAGACACTACGGTAAACTTCCTCATAGCAATCTGGCCTTTCTGATATCTGGTT      | 316 |
| Db  | 81        | AsnGlnLysThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal     | 100 |
| QY  | 317       | GTGCTGTTTGTCTCACCTTTTCACACTGACGCTGCTCTCTGGATCAGTGGAGTTTGGC    | 376 |
| Db  | 101       | ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly  | 120 |
| QY  | 377       | AAAGTCATGTGCCATATTATGCTTTTCTTCAATGTGTCTCAGTTTGTGTTTCAACTTFA   | 436 |
| Db  | 121       | LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu  | 140 |
| QY  | 437       | ATTTTAATATCAATTGCCATTGTCAGGTATCATATGATAAAACATCCCATATCTAATAAT  | 496 |
| Db  | 141       | IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn  | 160 |
| QY  | 497       | TTAACAGCAAAACATGGCTACTTCTGTAGTACTGTCTGGACACTAGGTTTGGCATC      | 556 |
| Db  | 161       | LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle  | 180 |
| QY  | 557       | TGTTCTCCCTCCAGTGTTCACAGTCTGTGGAACTTCAAGAAACATTTGGTTTCAGCA     | 616 |
| Db  | 181       | CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla  | 200 |
| QY  | 617       | TTCTCTGAGCAGCAGGTATTTATGTGTAGTCATGCCCATCTGATTTCACAGAAATGCC    | 676 |
| Db  | 201       | LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla  | 220 |
| QY  | 677       | TTTACTATCTCTTTATTTGCTAGTTCAGTATATTCCTGCCCTTAGTTTGTCTTACTGTAAT | 736 |
| Db  | 221       | PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer     | 240 |
| QY  | 737       | CATCAAGTGTCTGCAGAAAGTATAAGCTGTGATTGTTCCAAAGAAAGAAACAGACTTGA   | 796 |
| Db  | 241       | HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu  | 260 |
| QY  | 797       | GAAATGAGATGATCAACTTAATCTCTTCATCATCCAAAGAGTGGCTCAGGTGAA        | 856 |
| Db  | 261       | GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys  | 280 |
| QY  | 857       | CTCTCTGGCAGCCATAAATGGAGTTTATTCATTTCATCAAAAACACAGAGAAGATATAG   | 916 |
| Db  | 281       | LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer     | 300 |
| QY  | 917       | AAGAAGACAGCATGTGTGTTTACTCTCCAGAAAGACCTTCTCAAGAGAACCACTCAGA    | 976 |
| Db  | 301       | LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg  | 320 |

QY 977 ATACTCCAGAAAACCTTTGGCTCTGTAAGAGCTAGCTCTCTTCATCCAGTAAGTTGATA 1036  
 |||||  
 Db 321 IleLeuProGluAsnPhcGlySerValArgSerGlnLeuSerSerSerLysPheIle 340  
 |||||  
 QY 1037 CCAGGGGCCCCACCTTGTCTTGAGATAAAACCTGAGAGAAATTCAGATGTTTCATGAATTG 1096  
 |||||  
 Db 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360  
 |||||  
 QY 1097 ACAGTAAACAGTCTCTTACAGAGATAAAAGAGATCTCGAAGTGTCTTACAGACTG 1156  
 |||||  
 Db 361 ArgValLysArgSerValThrArgIleLysArgSerArgSerValPheTyrArgLeu 380  
 |||||  
 QY 1157 ACCATACATGATATTAGTATTGCTGTTAGTTGGATGCCACTACACCTTTTCATGTGGTA 1216  
 |||||  
 Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400  
 |||||  
 QY 1217 ACTGATTTTATGACAACTTATTTCATTAATAGGCATTTCAAGTTGGTGTATTGCAATTTGT 1276  
 |||||  
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420  
 |||||  
 QY 1277 CATTTGTTGGGCATGATCTCTGTTGCTGTTAATCCAAATTCATATGCGTTTCTTAATAAT 1336  
 |||||  
 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
 |||||  
 QY 1337 GGGATTAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG 1381  
 |||||  
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455  
 |||||  
 RESULT 5  
 ID AAY57461  
 XX AAY57461 standard; protein; 455 AA.  
 AC AAY57461;  
 DT 25-FEB-2000 (first entry)  
 XX Human hippocampal Y5 receptor.  
 DE Y5 receptor; feeding behaviour; food consumption; obesity; bulimia;  
 KW anorexia; neuro peptide; genetic engineering.  
 XX Homo sapiens.  
 XX US968819-A.  
 XX PD 19-OCT-1999.  
 XX PF 01-DEC-1995; 95US-00566096.  
 XX PR 02-DEC-1994; 94US-00349025.  
 XX PA (SYNA-) SYNAPTIC PHARM CORP.  
 XX Walker MW, Branchek T, Gerald CPG, Weinshank RL;  
 XX WPI; 1999-590415/50.  
 XX DR N-PSDB; AAZ39046.  
 XX PT Nucleic acid encoding a human neuropeptide Y receptor useful in genetic  
 XX engineering.  
 XX Disclosure; Fig 6; 87pp; English.

CC receptor can also be determined using cells expressing the receptor. The  
 CC effect of drugs on the Y5 receptor and whether they act as agonists or  
 CC antagonists can also be detected with these cells  
 XX  
 SQ Sequence 455 AA;  
 Alignment Scores: 1 34e-253 Length: 455  
 Pred. No.: 2385.00 Matches: 455  
 Score: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 96.17% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-771-956-4 (1-1406) x AAY57461 (1-455)  
 QY 17 ATGCTCTTTTATCCAGCAGACTATATATGAGATTAGAGCTCGACGAGTATTATAAC 76  
 |||||  
 Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20  
 |||||  
 QY 77 AAGACACTTGGCCACAGAGATAATATCTGCTGCTCCACTCGGAATTCGATTTCACAGTCTGG 136  
 |||||  
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40  
 |||||  
 QY 137 GATGACTATAAAAGCAGTGTAGATGACTTACAGTATTTTCTGATTGGGCTCTATACATTT 196  
 |||||  
 Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60  
 |||||  
 QY 197 GTAAGTCTTCTGGCTTTATGGGGAATCTACTATTATTAATGGCTCTCATGAAAAGCGT 256  
 |||||  
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80  
 |||||  
 QY 257 AATCAGAGACTACGGTAAACTTCTCATAGCAATCTGGCTTTCTGATATCTTGGTT 316  
 |||||  
 Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100  
 |||||  
 QY 317 GGTGCTTTTGTCTACCTTTTCACACTGAGCTGTCTGCTGGATCAGTGGATTTGGC 376  
 |||||  
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120  
 |||||  
 QY 377 AAGTCACTGTGCATATTATGCTTTTCTCAATGTGTGTCAGTTCGTTTCAACTTTA 436  
 |||||  
 Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140  
 |||||  
 QY 437 ATTTTAATATCAATGTCAGGTATCATATGATAAACAATCCCATATCTAATAAT 496  
 |||||  
 Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160  
 |||||  
 QY 497 TTAACAGCAAAACCATGGCTACTTTCTGATAGCTACTGTCTGACACTAGGTTTGGCATC 556  
 |||||  
 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180  
 |||||  
 QY 557 TGTCTCCCTTCCAGTCTTTTCACAGTCTTCTGGAACCTCAAGAAACATTTGGTTCAGCA 616  
 |||||  
 Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200  
 |||||  
 QY 617 TTGCTGACGACGAGTATTATTATGTTGAGTCATGGCCATCTGATTATACAGATTTGCC 676  
 |||||  
 Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220  
 |||||  
 QY 677 TTTACTATCTCTTTTATTGCTAGTTAGTTATTTCTGCCCTTAGTTTGTCTTACTGTAGT 736  
 |||||  
 Db 221 PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240  
 |||||  
 QY 737 CATCAAGTCTGTCAGAGATATAAGCTGTGGATTGTCACAAAGAAACAGACTTTGAA 796  
 |||||  
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260  
 |||||  
 QY 797 GAAATGAGATGATCAACTTAACCTTCTCATCCATCCAAAAGAGTGGGCTCAGGTGAAA 856  
 |||||  
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280  
 |||||  
 QY 857 CTCTGCGGCCCATATAAATGGAGTTATTTCATTCATAAAAAACACAGAAAGATATAGC 916  
 |||||

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Db      281 LeuSerGlySerHisLysTrpSerTyrSerPheLeuLysHisArgArgTyrSer 300
QY      917 AAGAGACACATGTGTGTTTACCTGCTCCAGAAAGACCTTCCAGAGAACCCACTCCAGA 976
Db      301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
QY      977 ATACTTCCAGAAACCTTTGGCTCTGTAAAGAGTCAGCTCTCTTCATCCAGTAAGTTTCATA 1036
Db      321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheLeu 340
QY      1037 CCAGGGGTCCTCCACTGCTTTGAGATAAAACCTGAGAGAAATTCAGATGTTCAATG 1096
Db      341 ProGlyValProThrCysPheGluIleLysProGluAsnSerAspValHisGluLeu 360
QY      1097 AGAGTAAACCTTCTGTACAGATAAAGAGAGATCTCGAAGTGTTTCTACAGACTG 1156
Db      361 ArgValLysArgSerValThrArgLleLysLysArgSerArgSerValPheTyrArgLeu 380
QY      1157 ACATACTGATATAGTATTGCTGTAGTTGATGCCACTACACCTTTTCCATGTTGTA 1216
Db      381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
QY      1217 ACTGATTTTAATGACAACTTATTTCAAATAGGCATTTCAAGTTGGTGATTGCAATTTGT 1276
Db      401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
QY      1277 CATTGTTGGGATGATGCTCTGCTGTTCTTAATCCAAATCTATATAGGGTTCTTAATAAT 1336
Db      421 HisLeuLeuGlyMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
QY      1337 GGGATTAAGCTGATTTAGTGTGCTTATACACTGCTTCATATG 1381
Db      441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 6
ID AAE08002 standard; protein; 455 AA.
AC AAE08002;
DT 01-NOV-2001 (first entry)
XX Human neuropeptide Y5 (NPY5) receptor.
XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein; transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy; Huntington's disorder; Parkinson's disorder; eating disorder; seizure; locomotor; anxiety disorder; limbic seizure; tranquilliser; human.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 1..50
FT /note= "N-terminal extracellular domain"
FT Domain 51..71
FT /note= "First TM domain"
FT Domain 72..84
FT /note= "First intracellular loop domain"
FT Domain 85..105
FT /note= "Second TM domain"
FT Domain 106..125
FT /note= "First extracellular loop domain"
FT Domain 126..145
FT /note= "Third TM domain"
FT Domain 147..167
FT /note= "Second intracellular loop domain"
FT Domain 168..188
FT /note= "Fourth TM domain"
FT Domain 189..220
FT /note= "Second extracellular loop domain"
FT Domain 221..241
FT /note= "Fifth TM domain"

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FT Domain 242..378
FT /note= "Third intracellular loop domain"
FT Domain 379..401
FT /note= "Sixth TM domain"
FT Domain 402..414
FT /note= "Third extracellular loop domain"
FT Domain 415..438
FT /note= "Seventh TM domain"
FT Domain 439..455
FT /note= "C-terminal intracellular domain"
XX W0200155103-A2.
XX 02-AUG-2001.
XX 29-JAN-2001; 2001WO-US0002804.
XX 28-JAN-2000; 2000US-0178652P.
XX (NEUR-) NEUROGEN CORP.
XX Bennett M, Brodbeck R, Krause J;
XX WPI; 2001-514543/56.
XX N-PSDB; AAD14734.
XX New chimeric receptor proteins comprising a single polypeptide chain of amino acids, useful as targets for drug actions, and as basis for drug discovery and development.
XX Example 2; Page 55-56; 72pp; English.
XX The present invention relates to chimeric neuropeptide Y (NPY) receptors. The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPY5 receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is human NPY5 receptor
XX Sequence 455 AA;
SQ
Alignment Scores:
Pred. No.: 1,346-253 Length: 455
Score: 2385.00 Matches: 455
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.17% Indels: 0
DB: 4 Gaps: 0
US-09-771-956-4 (1-1406) x AAE08002 (1-455)
QY 17 ATGCTTTTATCCAAAGCAGACTATATATGGATTTAGAGTCGACGAGTATTATAAC 76
Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTrpAsn 20
QY 77 AAGACACTTGGCCACAGAGATAATATCTGCTGCCACTCGGAATTTCTGATTTCCCACTCGG 136
Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40
QY 137 GATGACTATAAAGCAGCTAGATGACTACAGTATTTTCTGATTTGGGCTCTATACATTT 196
Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
QY 197 GTAAGTCTTTTGGCTTTATGGGAATCTACTTATTTTAATGGTCTCATGAAAACGCT 256
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuLeuMetAlaLeuMetLysLysArg 80
QY 257 AATCAGACACTACGGTAAACTTCTCATAGCAATCTGGCTTTTCTGATATCTTCTT 316

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QY 1037 CCAGGGTCCCCCTTCCTTTGAGATAAAACCTGAAGAAAATTCAGATGTCATGAATG 1096  
 Db 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360  
 QY 1097 AGACTAAACGTTCTGTTTACAGAATAAAAAAGAGATCTCGAAGTGTGTTTCTACAGACTG 1156  
 Db 361 ArgValLysArgSerValThrArgLleLysLysArgSerArgSerValPheTyrArgLeu 380  
 QY 1157 ACCATCTGATATTAAGTATTGCTGTGTAGTTGGATGGCCATACACCTTTTCCATGTGGTA 1216  
 Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400  
 QY 1217 ACTGATTTTAATGACAAATCTATTTCAAATAGGCAATTCAGTTGGTGTATTGCAATTTGT 1276  
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420  
 QY 1277 CATTTGTTGGCATGATGCTGTTGCTTCTTAATCCAAATTCATATGCGTTTCTTAATAAT 1336  
 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
 QY 1337 GGGATTAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG 1381  
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455  
 RESULT 8  
 ABB79510  
 ID ABB79510 standard; protein; 455 AA.  
 XX AC ABB79510;  
 XX DT 23-SEP-2002 (first entry)  
 XX DE Human neuropeptide Y5 receptor.  
 XX KW Neuropeptide Y5; NPY; NPY5; receptor; human; antagonist; anorectic;  
 KW antiinflammatory; nootropic; neuroprotective; cardiovascular;  
 KW hypotensive; antidiabatic; psychiatric; anticonvulsant; cardiant;  
 KW cerebroprotective; antidepressant; haemostatic; tranquillizer;  
 KW neuroleptic; analgesic; antianginal; nephrotropic; uropathic;  
 KW gastrointestinal; antiaschmatic.  
 XX OS Homo sapiens.  
 XX FN WO200248152-A2.  
 XX PD 20-JUN-2002.  
 XX 11-DEC-2001; 2001WO-US047863.  
 XX 12-DEC-2000; 2000US-0254990P.  
 XX (NEUR-) NEUROGEN CORP.  
 XX Bakhavatchalam R, Bium CA, Brielmann HL, Darrow JW;  
 PI De Lombaert S, Hutchison A, Tran J, Zheng X, Elliott RL, Hammond M;  
 DR WPI: 2002-547845/58.  
 DR N-PSDB; ABN84252.  
 XX  
 FT New substituted spiro(isbenzofuran-1,4'-piperidin)-3-one or 3H-  
 FT spiro(isbenzofuran-1,4'-piperidine, useful for treating, e.g. eating  
 FT disorder, psychiatric, cardiovascular disorder or diabetes.  
 XX  
 XX Example 675; Page 129-130; 134pp; English.  
 XX  
 CC The present sequence is the protein sequence for the human neuropeptide  
 CC Y5 (NPY5) receptor. In an example from the invention, chimeric receptors  
 CC including human NPY5 receptor sequences were constructed, and used to  
 CC assay the binding activity of compounds of the invention. Substituted  
 CC spiro(isbenzofuran-1,4'-piperidin)-3-ones and 3H-spiro(isbenzofuran-1,4'-  
 CC piperidines capable of modulating NPY5 receptor activity are provided.  
 CC Such compounds may be used to modulate ligand binding to NPY5 receptors  
 CC

CC in vivo or in vitro, and are particularly useful in the treatment of a  
 CC variety of disorders, e.g. eating disorders such as obesity or bulimia,  
 CC psychiatric disorders, diabetes and cardiovascular disorders such as  
 CC hypertension, in humans and animals

XX  
 SQ Sequence 455 AA;

#### Alignment Scores:

Pred. No.: 1.34e-253 Length: 455  
 Score: 2385.00 Matches: 455  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 96.17% Indels: 0  
 DB: 5 Gaps: 0

US-09-771-956-4 (1-1406) x ABB79510 (1-455)

|    |     |                 |                |                 |                  |                  |
|----|-----|-----------------|----------------|-----------------|------------------|------------------|
| QY | 17  | ATGTCCTTTTATTC  | CAAGCAGGACTATA | TATGATTTAGAGCTC | GAGAGTATTATAAC   | 76               |
| Db | 1   | MetSerPheTyrSer | LysGlnAspTyr   | AsnMetAspLeu    | GluLeuAspGluTyr  | Asn 20           |
| QY | 77  | AAGACACTTGCAC   | AGAGAATAACTGCT | CCACTCGGAATTC   | GATTTCCCACTCGG   | 136              |
| Db | 21  | LysThrLeuAla    | ThrGluAsnThr   | AlaAlaThrArg    | AsnSerAspPhe     | ProValTyr 40     |
| QY | 137 | GATGACTATAAAG   | CAGGTAGAGTAC   | TACAGATTCTTCT   | GATGGCTCTACATTT  | 196              |
| Db | 41  | AspAspTyrLys    | SerSerValAsp   | AspLeuGlnTyr    | PheLeuIleGlyLeu  | TyrThrPhe 60     |
| QY | 197 | GTAAGTCTTCTTG   | CGTTTATGGGAAT  | CTACTTATTTTAA   | TGGCTCTCATGAAA   | ACGCT 256        |
| Db | 61  | ValSerLeuLeu    | GlyPheMetGly   | AsnLeuLeuLeu    | MetAlaLeuMetLys  | LeuArg 80        |
| QY | 257 | AATCAGAGACTAG   | CTAAAGCTTCTCA  | TAGGCAATCTG     | CGCTTTCTGATATCT  | TGGTT 316        |
| Db | 81  | AsnGlnLysThr    | ValAsnPheLeu   | IleGlyAsnLeu    | AlaPheSerAspIle  | LeuVal 100       |
| QY | 317 | GTGCTGTTTGTCT   | CACCTTTTCCACT  | GTGCTGCTGCT     | GTGTCATCAGTGGAT  | TTGGC 376        |
| Db | 101 | ValLeuPheCys    | SerProPheThr   | LeuThrSerVal    | LeuLeuAspGlnTyr  | MetPheGly 120    |
| QY | 377 | AAAGTCATGCGCA   | TATATGCCCTTTT  | CTCAATGTGTGTC   | AGTTTGGTTTCAAC   | TTTA 436         |
| Db | 121 | LysValMetCys    | HisIleMetPro   | PheLeuGlnCys    | ValSerValLeuVal  | SerThrLeu 140    |
| QY | 437 | ATTTTAATATCA    | ATTGCCATTTGCA  | GTATCATATGATA   | ATAAACATCCATATCT | ATAAT 496        |
| Db | 141 | IleLeuIleSer    | IleAlaIleVal   | ArgTyrHisMet    | IleLysHisProIle  | SerAsnAsn 160    |
| QY | 497 | TTAACAGAAACCA   | TGGCTACTTTCTC  | ATAGCTACTGCT    | CTGCGACACTAGGTT  | TTGCCATC 556     |
| Db | 161 | LeuThrAlaAsn    | HisGlyTyrPhe   | LeuIleAlaThr    | ValTyrThrLeuGly  | PheAlaIle 180    |
| QY | 557 | TGTTCTCCCTCC    | AGGTTTCAAGCTT  | GTGGACTTCAAGA   | ACATTTGCTTCAGCA  | 616              |
| Db | 181 | CysSerProLeu    | ProValPheHis   | SerLeuValGlu    | LeuGlnGlnThrPhe  | GlySerAla 200    |
| QY | 617 | TTGCTGAGCAGC    | AGGATTTATGTG   | TGTGAGTCTATGC   | CATCTGATTCATACA  | GAGAAATGCC 676   |
| Db | 201 | LeuLeuSerSer    | ArgTyrLeuCys   | ValGluSerTyr    | ProSerAspSerTyr  | ArgIleAla 220    |
| QY | 677 | TTTACTATCTCT    | TATTTAGTTCAGT  | ATATTCGCTTCT    | GTCTTACTGTAAGT   | 736              |
| Db | 221 | PheThrIleSer    | LeuLeuValGln   | TyrIleLeuPro    | LeuValCysLeuThr  | ValSer 240       |
| QY | 737 | CATACAGTCTCT    | GCAGAGTATAAG   | CTGTGGATTGTCC   | CAACAAAGAAAAC    | AGACTTTGAA 796   |
| Db | 241 | HisThrSerVal    | CysArgSerIle   | SerCysGlyLeu    | SerAsnLysGlu     | AsnArgLeuGlu 260 |
| QY | 797 | GAATAATCAGAT    | CACTCACTTCACT  | TCCATCCATCCAA   | AAAAGAGTGGGCTC   | AGGTGAAA 856     |
| Db | 261 | GluAsnGluMet    | IleAsnLeuThr   | LeuHisProSer    | LysLysSerGlyPro  | GlnValLys 280    |

|    |      |               |              |               |                 |                    |
|----|------|---------------|--------------|---------------|-----------------|--------------------|
| QY | 857  | CTCTCTGGCAGC  | CAATAAATGGAG | TTATTTCATTCAT | CAAAAAACACAGA   | AGATATAGC 916      |
| Db | 281  | LeuSerGlySer  | HisLysTyrSer | TyrSerPheIle  | LysHisArgArgTyr | Ser 300            |
| QY | 917  | AAGAAGACAGCA  | CTGTGTGTACCT | CTCCAGAAAGAC  | CTTCTCAAGAGA    | ACCACCTCCAGA 976   |
| Db | 301  | LysLysThrAla  | CysValLeuPro | AlaProGluArg  | ProSerGlnGlu    | AsnHisSerArg 320   |
| QY | 977  | ATACTTCCAGAA  | AACTTTGGCTCT | GTAAAGATCAG   | CTCTCTTCATCC    | AGTAAGTTCATA 1036  |
| Db | 321  | IleLeuProGlu  | AsnPheGlySer | ValArgSerGln  | LeuSerSerSer    | SerLysPheIle 340   |
| QY | 1037 | CCAGGGTCCCACT | TGCTTTGAGATA | AAAAACCTGAGA  | AAAAAATTCAGAT   | GTTCATGAATG 1096   |
| Db | 341  | ProGlyValPro  | ThrCysPheGlu | IleLysProGlu  | GluAsnSerAsp    | ValHisGluLeu 360   |
| QY | 1097 | AGAGTAAACGTT  | CTGTTTACAAGA | TAAATAAAGAGAT | CTCGAAGTGT      | TTTTCTACAGCTG 1156 |
| Db | 361  | ArgValLysArg  | SerValThrArg | IleLysLysArg  | SerArgSerVal    | PheTyrArgLeu 380   |
| QY | 1157 | ACCATACTCAT   | ATTAGTATTGCT | GTAGTTGGATG   | CCCACTACACCT    | TTTTCATCTGTA 1216  |
| Db | 381  | ThrIleLeuIle  | LeuValPheAla | ValSerTyrMet  | ProLeuHisLeu    | PheHisValVal 400   |
| QY | 1217 | ACTGATTTTAA   | TGACAACTTAT  | TTTCAATAGGCA  | TTTCAAGTTGGT    | TGTTGCAATTTGT 1276 |
| Db | 401  | ThrAspPheAsn  | AsnLeuIleSer | AsnArgHisPhe  | LysLeuValTyr    | CysIleCys 420      |
| QY | 1277 | CATTGTTGGGCA  | TGATGCTGTTG  | TCTTAAATCAAT  | TCTATATGGGTT    | TTCTTAATAAT 1336   |
| Db | 421  | HisLeuLeuGly  | MetMetSerCys | CysLeuAsnPro  | IleLeuTyrGly    | PheLeuAsnAsn 440   |
| QY | 1337 | GGGATTAAGCT   | GTATAGTTAGT  | GTCCCTTATACA  | CTCTCTTTCATATG  | 1381               |
| Db | 441  | GlyIleLysAla  | AspLeuValSer | LeuIleHisCys  | LeuHisMet       | 455                |

#### RESULT 9

|    |   |                            |
|----|---|----------------------------|
| ID | AAO23266  | standard; protein; 455 AA. |
| XX | AAO23266;   |                            |
| AC | AAO23266;   |                            |
| XX | 25-SEP-2003 (first entry)   |                            |
| DT | Human neuropeptide Y5 receptor (NPY5) protein.                            |                            |
| DE | Neuropeptide Y5; receptor; NPY5; 2-cyclohexyl-4-phenyl-1H-imidazole; NPY; |                            |
| KW | appetite regulation; feeding disorder; obesity; bulimia; diabetes;        |                            |
| KW | psychiatric; cardiovascular; hypertension; cerebral infarction; epilepsy; |                            |
| KW | schizophrenia; depression; angina; sudden cardiac death; vasospasm;       |                            |
| KW | arrhythmia; urinary incontinence; Crohn's disease; asthma; neuroleptic;   |                            |
| KW | antiinflammatory; nootropic; vasotropic; anticonvulsant; uropathic;       |                            |
| KW | human.  |                            |
| XX | Homo sapiens.   |                            |
| OS | EP1306085-A1.   |                            |
| PN | 02-MAY-2003.  |                            |
| XX | 21-OCT-2002; 2002EP-00023469.   |                            |
| XX | 23-OCT-2001; 2001US-0348974P.   |                            |
| XX | (NEUR-) NEUROGEN CORP.  |                            |
| XX | Blum CA, Brielmann HL, De Lombaert S, Zheng X;                            |                            |
| XX | WPI; 2003-543553/52.  |                            |
| DR | N-PSDB; AAL56583.   |                            |
| XX | New 2-cyclohexyl-4-phenyl-1H-imidazole derivatives are modulators of      |                            |
| PT | neuropeptide Y5 receptor activity, useful for treating e.g. eating or     |                            |



PT psychiatric disorders.

XX PS Example 10; Page 39-41; 63pp; English.

XX CC This invention relates to novel ligands (derivatives of 2-cyclohexyl-4-phenyl-1H-imidazole) for the neuro-peptide Y5 (NPY5) receptor. The NPY5 receptor mediates a variety of physiological effects and is involved in appetite regulation, hormone release and blood pressure. Ligands that modulate the NPY5 receptor inhibit or enhance NPY binding such that they can be used to treat a variety of conditions including feeding disorders (obesity and bulimia), psychiatric disorders, diabetes and cardiovascular diseases such as hypertension. Further uses relate to the treatment of cerebral infarction, epilepsy, schizophrenia, depression, angina, sudden cardiac death, vasospasm, arrhythmia, urinary incontinence, Crohn's disease and asthma. As such these ligands can be described variously as neuroleptic, anti-inflammatory, nootropic, vasotropic, anticonvulsant and uropathic. This polypeptide sequence is the human neuro-peptide Y5 (NPY5) receptor protein of the invention

XX SQ Sequence 455 AA;

Alignment Scores:

Pred. No.: 1,348-253 Length: 455  
Score: 2385.00 Matches: 455  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 96.17% Indels: 0  
DB: 6 Gaps: 0

US-09-771-956-4 (1-1406) X AAO23266 (1-455)

QY 17 ATGCTTTTATCCAGCAGACATTAATATGAGATTAGAGCTGCGAGTATTAAC 76  
DB 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20  
QY 77 AAGACCTGCCACAGAGATAATCTGCTGCACTCGGAATCTCGATTTCCAGTCTGG 136  
DB 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40  
QY 137 GATGACTATAAAGCAGGTAGATGATCAGTATGATTTTCTGATGGCTCTATACATTT 196  
DB 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60  
QY 197 GTAAGCTCTTGGCTTTATGGGAATCTACTATTATTTAATGGCTCTCATGAAAAGCGT 256  
DB 61 ValSerLeuLeuGlyPheMetClyAsnLeuLeuLeuLeuMetAlaLeuMetLysLysArg 80  
QY 257 AATCAGAGACTACGGTAAACTTCTCATAGCAATCTGGCTTTTCTGATATCTGGTT 316  
DB 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100  
QY 317 GTGCTGTTTGTCTACCTTTCACATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 376  
DB 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuLeuLeuLeuLeuLeu 120  
QY 377 AAGTCAATGTCATATTATGCTTTCTTCAATGTGTGTGCTGCTGCTGCTGCTGCTGCT 436  
DB 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140  
QY 437 ATTTAATATCAATGTCATGTCAGGTATCATATGATAAACAATCCCATATCTTAATAT 496  
DB 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160  
QY 497 TTAACGACAAACCATGGTACTTTCTGATAGCTACTGCTGACACTAGTGTGGTTCATC 556  
DB 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrPheLeuGlyPheAlaIle 180  
QY 557 TGTCTCCCTCCAGTCTTTCACAGTCTTGGGAACCTCAAGAAATTTGGTTCAGCA 616  
DB 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheCysLeuAla 200  
QY 617 TTGCTGACGACGAGTATTTATGTTGAGTCAATGCGCATCTGATTCATCAGAAATGCC 676

DB 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220  
QY 677 TTTACTATCTCTTTATTGCTAGTTCAGTATATCTGCGCTTGTGCTTGTCTTACTGTAAGT 736  
DB 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240  
QY 737 CATACAGTGTCTGAGAGATATAAGCTGTGATGTTCCAAACAAGAAAACAGACTTGAA 796  
DB 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260  
QY 797 GAAATGTAGATGATCAACTTAACCTTCTCATCCATCCAAAAGAGTGGGCTCCAGTGAAA 856  
DB 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValys 280  
QY 857 CTCTCTGGCAGCCATAAATGAGGTATTTCATTCATCAAAAACACAGAGAGATATAGC 916  
DB 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300  
QY 917 AAGAAAGACAGCATGTGTGTATTACCTGCTCCAGAAAAGACCTTCTCAAGAGAACCCTCCAGA 976  
DB 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320  
QY 977 ATACTTCAGAAAACCTTTGGCTGTGTAAGAGTGCAGCTCTCTTCATCCAGTAAGTTGATA 1036  
DB 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340  
QY 1037 CCAGGGGTCCCGACCTGCTTTGAGATMAAACCTCAAGAAAATTCAGATGTTTCATGAATTG 1096  
DB 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360  
QY 1097 AGAGTAAAACGTTCTGTACAGAAATAAAGAGATCTCGAAGTGTTCAGACTGTTTACAGACTG 1156  
DB 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380  
QY 1157 ACCATACCTGATATTAGTATTGCTGTGTAGTTGGATGCCACTACACCTTTTCCATGTGGTA 1216  
DB 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400  
QY 1217 ACTGATTTTATGACAATCTTATTTCAAATAGGACTTCAAGTTGGTGTATGCAATTGT 1276  
DB 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420  
QY 1277 CATTGTGGGCGATGATGCTGCTGTGTCTTAATCCAAATTCATATGCGTGTTCCTTAATAT 1336  
DB 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
QY 1337 GGGATTAAGCTGATTTAGTGTCCCTTATACACTGCTTCTCATATG 1381  
DB 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 10

AD029564  
ID AD029564 standard; protein; 455 AA.

AC AD029564;

DT 29-JUL-2004 (first entry)

DE Human GPCR NP5R, SEQ ID NO:666.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
XX transgenic mouse; neurological disorder; adrenal gland disorder;  
XX colon disorder; intestinal disorder; cardiovascular disorder;  
XX muscular disorder; blood disorder; immune disorder; bone disorder;  
XX joint disorder; metabolic disorder; nutritive disorder; cancer;  
XX kidney disorder; liver disorder; lung disorder; breast disorder;  
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;  
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
XX thymus disorder; thyroid disorder; antiparkinsonian; aminic;  
XX cytostatic; antiinflammatory; vasotropic; antianginal; antirhythmic;  
XX CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
XX viricide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;  
XX dermatological; antiulcer; antithyroid; antiallergic; anorectic;

immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 receptor.  
 Homo sapiens.  
 WO2004040000-A2.  
 13-MAY-2004.  
 09-SEP-2003; 2003WO-US028226.  
 09-SEP-2002; 2002US-0409303P.  
 09-APR-2003; 2003US-0461329P.  
 (PRIM-) PRIMAL INC.  
 Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li P;  
 Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
 WPI: 2004-390329/36.  
 N-PSDB; ADO30001.  
 Novel mammalian G protein coupled receptors, useful for identifying  
 compounds that modulates diagnosing and treating disease condition  
 associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 pectoris, Parkinson's disease.  
 Claim 151; SEQ ID NO 666; 542pp; English.  
 The invention relates to human and mouse G protein-coupled receptors  
 (GPCRs) and nucleic acids encoding them. The invention also relates to  
 sequences at least 90% identical to the GPCR proteins and nucleic acids  
 of the invention; methods of treating, preventing or diagnosing diseases  
 associated with GPCRs of the invention; methods of screening for  
 compounds useful in the treatment of GPCR-related diseases; a transgenic  
 mouse comprising a GPCR gene of the invention; a mouse comprising a  
 mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 from the transgenic mice; kits comprising several mice, each of which has  
 a mutation in a different GPCR gene of the invention; and kits comprising  
 probes which hybridize to GPCR polynucleotides of the invention. The  
 invention further discloses variants of the GPCR polypeptides and vectors  
 comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 be used in the diagnosis, treatment or prevention of a wide variety of  
 diseases including neurological disorders (e.g., Alzheimer's disease,  
 depression, diabetic neuropathy, Parkinson's disease or schizophrenia),  
 disorders of the adrenal gland; disorders of the colon or intestine  
 (e.g., Crohn's disease, diarrhea, food poisoning or irritable bowel  
 syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 myocardial infarction); muscular disorders; blood disorders (e.g.,  
 anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 thyroid (e.g., cancers). The present sequence represents a GPCR of the  
 invention. Note: The full sequence data for this patent did not form part  
 of the printed specification; those sequences not shown were obtained in  
 electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences.  
 Sequence 455 AA;

| Alignment Scores:      | 1.34e-253 | Length:       | 455 |
|------------------------|-----------|---------------|-----|
| Pred. No.:             | 2385.00   | Matches:      | 455 |
| Score:                 | 100.00%   | Conservative: | 0   |
| Percent Similarity:    | 100.00%   | Mismatches:   | 0   |
| Best Local Similarity: | 96.17%    | Indels:       | 0   |
| Query Match:           | 8         | Gaps:         | 0   |

US-09-771-956-4 (1-1406) x ADO29564 (1-455)

```

Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
QY 1157 ACCAATCTGATATAGTATTGCTGTAGTGTGAGTGCACCTACACCTTTTCCATGTGTA 1216
Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
QY 1217 ACTGATTTTAAATGACAACTTATTTTCAAAATAGGCATTTCAAGTTGGTGTATTGCAATTTGT 1276
Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
QY 1277 CATTTCTTGGGCGATGATGCTGCTGTCTTAATCCAAATCTATATGGGTTTCTTAATAT 1336
Db 421 HisLeuLeuGlyMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
QY 1337 GGGATTAAGCTGATTAGTGTCCCTTATACACCTGCTCTTCATATG 1381
Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 11
AAE08016
ID AAE08016 standard; protein; 455 AA.
AC
XX AAE08016:
XX
DT 01-NOV-2001 (first entry)
DE African green monkey (AGM) neuropeptide Y5 (NPY5) receptor.
XX
KW Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein; transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KW locomotor; anxiety disorder; limbic seizure; tranquilizer;
KW african green monkey; AGM.
XX
OS Cercopithecus aethiops.
XX
PN WO200155103-A2.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US002804.
XX
PR 28-JAN-2000; 2000US-0178652P.
XX
PA (NEUR-) NEUROGEN CORP.
XX
PI Bennett M, Brodbeck R, Krause J;
XX
WPI: 2001-514543/56.
DR N-PSDB; AAD14746.
XX
PT New chimeric receptor proteins comprising a single polypeptide chain of amino acids, useful as targets for drug actions, and as basis for drug discovery and development.
XX
PS Example 2; Page 70-72; 72pp; English.
XX
CC The present invention relates to chimeric neuropeptide Y (NPY) receptors. The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPY5 receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is african green monkey (AGM) NPY5 receptor
SQ Sequence 455 AA;
XX
Alignment Scores:

```

```

Pred. No.: 2,83e-252 Length: 455
Score: 2373.00 Matches: 452
Percent Similarity: 99.78% Conservative: 2
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 95.69% Indels: 0
DB: 4 Gaps: 0

US-09-771-956-4 (1-1406) x AAE08016 (1-455)
QY 17 ATGCTCTTTTATCCAGCAGGACTATATATGATGATGAGTCCGACGAGTATATTAAC 76
Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
QY 77 AAGACACTTGGCCACAGAGAATAATACTGCTGCCACTCGGAATTTCTGATTTCCCACTGCG 136
Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaThrArgAsnSerAspPheProValTrp 40
QY 137 GATGACTATAAAGCAGGATGTAGATCAGTACAGTATTTTCTGATGGCTCTCATACATTT 196
Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
QY 197 GTAAGTCTTTCTTGGCTTTTATGGGAATCTACTTTATTTTAAATGGCTCTCATCAAAAGCGT 256
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
QY 257 AATCAGAGACTACGGTAAACTTCTCATAGGCATCTGGCCTTTCTGATATCTTGGTT 316
Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
QY 317 GTGCTGTCTTGGCTACCTTTTACACTGACGCTGCTCTTGTCTGGATCAGTGGATGTTGGC 376
Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
QY 377 AAAGTCATGTGCCATATTATGCTTCTTCAATGTGTGTCAGTTTGGTTCACACTTA 436
Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
QY 437 ATTTTAATATCAATTCCTCATGTTGTCAGGTATCATATGATAAACAATCCCAVATCTATAAT 496
Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
QY 497 TTAACAGCAACCATGGCTACTTCTGATAGTACTCTGACACTAGGTAGTTTGGCATC 556
Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
QY 557 TGTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACCTTCAAGAAACATTTGGTTCAGCA 616
Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200
QY 617 TTGCTGACGACGAGGTATTTATGTTGAGTCATGCGCATCTGATTCATACAGAAATGCC 676
Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
QY 677 TTTACTATCTCTTTATGCTAGTTTCAGTATATTCTGCGCTTAGTTTCTTACTGTAAGT 736
Db 221 PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
QY 737 CATACAGTGTCTGAGAGATATAAGCTGTGGATTGTCACAAAGAAACAGACTTGAA 796
Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
QY 797 GAAATGAGATGATCAACTTAACTCTTCATCCATCCAAAGAGCTGGGCTCAGGTGAA 856
Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerArgLysIleGlyProGlnValLys 280
QY 857 CTCTCTGGCAGCCATAAATAGGATTATTCATTCATCAAAAACACAGAGAGATATAGC 916
Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgTyrSer 300
QY 917 AAGAGACAGCATGTGTGTATTACCTGCTCCAGAAAGACTTCTCAAGAGAACCACTCCAGA 976
Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320

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QY 977 ATACTCCAGAAACTTTGGCTCTGTAGAGTCTAGCTCTCTCTCATCCAGTAAGTTCATA 1036  
 Db 321 ILLeuProGluAsnPhGlySerValArgSerGlnLeuSerSerSerlySPheile 340  
 QY 1037 CCAGGGGTCCTCCACTTGTCTTTCAGATATAAAGCTGAGAAATTCAGATGTTTCAGTAATG 1096  
 Db 341 ProGlyValProThrCysPheGluLeuLeysProGluGluAsnSerAspValHisGluLeu 360  
 QY 1097 AGAGTAAACGCTCTGTCTACAGAAATAAAGAGATCTCGAAGTGTCTTCTACAGACTG 1156  
 Db 361 ArgValLysArgSerValThrArgileLysLysArgSerArgSerValPheTyrArgLeu 380  
 QY 1157 ACCATACATGATATTAGTATTGCTGTTAGTGGATGCGACCTACACCTTTCCATGTCGTA 1216  
 Db 381 ThrIleLeuLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400  
 QY 1217 ACTGATTTTAATGACAATCTTATTTCAATAGGCAATTTCAAGTTGGTGTTATTCGATTGT 1276  
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysileCys 420  
 QY 1277 CATTTGTTGGGCATGATCTCTGTTGCTCTTAATCCAAATCTATATGTTGGTTCTTAATAAT 1336  
 Db 421 HisLeuLeuGlyMetSerCysLysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
 QY 1337 GGGATTAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG 1381  
 Db 441 GlyIleLysAlaAspLeuMetSerLeuIleHisCysLeuHisMet 455  
 RESULT 12  
 AAW27604  
 ID AAW27604 standard; protein; 445 AA.  
 AC AAW27604;  
 DT 14-APR-1998 (first entry)  
 DE Human neuropeptide Y receptor (NPY Y5).  
 KW Neuropeptide Y receptor Y5; NPY Y5; peptide YY; NPY/Y receptor; human;  
 KW neurotransmitter; antagonist; agonist; obesity; anorexia;  
 KW hyperlipidaemia; diabetes; gene therapy; transgenic animal.  
 OS Homo sapiens.  
 PN W09737998-A2.  
 PD 16-OCT-1997.  
 PF 08-APR-1997; 97WO-US005781.  
 PR 08-APR-1996; 96US-0014969P.  
 PA (FARB ) BAYER CORP.  
 PI Hu Y, Mccaleb ML, Bloomquist BT, Flores-Riveros JR, Cornfield LJ;  
 DR WPI; 1997-512637/47.  
 DR N-PSDB; AAT73602.  
 PT Nucleic acid molecule encoding neuro:peptide Y receptor - useful to  
 PT identify antagonists and agonists, e.g. treat obesity, diabetes,  
 PT hyperlipidaemia and anorexia.  
 XX Claim 2; Page 37-39; 49pp; English.

CC antagonists could be used to treat obesity and diabetes by reducing  
 CC appetite and food consumption, while agonists could be used to treat  
 CC anorexia  
 XX SQ Sequence 445 AA;  
 Alignment Scores:  
 Pred. No.: 1.56e-247 Length: 445  
 Score: 2330.00 Matches: 445  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.95% Indels: 0  
 DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x AAW27604 (1-445)

QY 47 ATGGATTAGAGCTCGACGAGTATTATAACAAGACACTTGCACAGAGATAATATCTGCT 106  
 Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20  
 QY 107 GCACCTCGGAATCTCGATTTCCAGTCTGGGATGACTATAAAGCAGTGTAGATCACTTA 166  
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40  
 QY 167 CAGTATTTTCTGATTGGGCTCTATACATTGTGAAGTCTTCTGGCTTTATGGGAATCTA 226  
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 QY 227 CTTATTTTAATGGCTCTCATGAAAAAGCCTAATCAGAAGACTACGGTAAACTTCCTCATA 286  
 Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeuIle 80  
 QY 287 GGCATCTGGCCCTTTCTGATATCTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 346  
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValLeuPheCysSerProPheThrLeuThr 100  
 QY 347 TCTGTCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 406  
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120  
 QY 407 CAATGTGTGTGAGTTTGTGGTTCACCTTTAATTTAATCAATTCATTCATTCATTCATTC 466  
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140  
 QY 467 CATATGATAAAACATCCCATATCTAATAATTAACAGCAAAACCATGGCTACTTCTGATA 526  
 Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160  
 QY 527 GCTACTGTCTGGACACTAGTTTGGTTCACATCTGTCTCCCTTCCAGTGTTCACAGTCTT 586  
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
 QY 587 GTGGAACCTCAAGAAACATTTGGTTCAGCATTTGTCAGCAGCAGCAGTATTTATGTTGAG 646  
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200  
 QY 647 TCATGGCCATCTGATTCATACAGAAATTCCTTTACTATCTCTTTATTGCTAGTTTCAGTAT 706  
 Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220  
 QY 707 ATTCCTGCTTGTGTTGCTTCTTACTGTAGTTCATACAGTGTCTGACAGCTATTAAGCTGT 766  
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
 QY 767 GGATTTGTCACAAAGAAACAGACTTTCAGCAAAATCAGATGATCAACTTAACCTTCATCAT 826  
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260  
 QY 827 CCATCCAAAAGAGTGGCCCTCAGTGAAACTCTCTGGCAGCCCATTAATGGAGTTATTCATCA 886  
 Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTrpSer 280  
 QY 887 TTCATCAAAAACACAGAAAGATATAGCAAGAACAGCATGTGTGTGTACCTGCTCCCA 946



QY 827 CCATCAAAAAGAGTGGGCTCAGTGAAACTCTCTGGCAGCCATAAATGGAGTTATTCA 886  
 Db 261 ProSerLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTrpSer 280  
 QY 887 TTCATCAAAAACACAGAGAGATATACACAGAGACAGAGATGCTGTACCTGCTCCA 946  
 Db 281 PheLeuLysHisGargArgTrpSerLysLysThrAlaCysValLeuProAlaPro 300  
 QY 947 GAAAGACCTTCTCAAGAGAACCACTCCAGATPACTTCCAGAAAACCTTTGGCTCTGTAAGA 1006  
 Db 301 GluArgProSerGlnGluAsnHisSerArgLleLeuProGluAsnPheGlySerValArg 320  
 QY 1007 AGTCAGCTCTCTCATCCAGTAAGTTTCATACAGGGGTCCCACTTGCTTTCAGATATAAA 1066  
 Db 321 SerGlnLeuSerSerSerLysPheLysPheLysValProThrCysPheGluLys 340  
 QY 1067 CCTGAAGAAAATTCAGATGCTTCATGAATTCAGAGTAAACAGTCTCTGTACAGATAAAA 1126  
 Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgLleLys 360  
 QY 1127 AAGAGATCTCGAAGTGTCTTACAGACTGACCATCTGATATAGTATTTGCTGTAGT 1186  
 Db 361 LysArgSerArgSerValPheTrpArgLeuThrLleLeuLleValPheAlaValSer 380  
 QY 1187 TGGATGCCACTACACTTTTCCATGCTGTGTAAGTATTTAATGACAATCTTATTTCAAT 1246  
 Db 381 TrpMetProLeuHisPheHisValValThrAspPheAsnAspAsnLeuLleSerAsn 400  
 QY 1247 AGGCATTTCAAGTGTGTATGCAATTTGTTGGCATCATGCTCTGTGTCTT 1306  
 Db 401 ArgHisPheLysLeuValTrpCysLysCysHisLeuLeuGlyMetSerCysCysLeu 420  
 QY 1307 RATCAAAATCTATATGGCTTCTTAATATGGATTAAGTATGATGCTCCTTATA 1366  
 Db 421 AsnProLleLeuTrpGlyPheLeuAsnAsnGlyLleLysAlaAspLeuValSerLeuLle 440  
 QY 1367 CACTGCTCTTCATATG 1381  
 Db 441 HisCysLeuHisMet 445  
 RESULT 14  
 AAY14554  
 ID AAY14554 standard; protein; 445 AA.  
 AC AAY14554;  
 XX  
 XX  
 DT 31-AUG-1999 (first entry)  
 XX Human neuropeptide Y5 receptor protein.  
 DE Human; neuropeptide Y; NPY; receptor; hypothalamus; antagonist; agonist;  
 XX obesity; diabetes; antibody; detection.  
 KW Homo sapiens.  
 OS  
 XX US919901-A.  
 FN 06-JUL-1999.  
 PD 08-APR-1996; 96US-00630118.  
 PF 08-APR-1996; 96US-00630118.  
 PR (FARB ) BAYER CORP.  
 XX Cornfield LJ, Flores-Riveros JR, Hu Y, Mccaleb ML, Bloomquist BT;  
 XX WPI; 1999-394648/33.  
 DR N-PSDB; AAX83197.  
 XX Neuropeptide Y receptor Y5 and related nucleic acid.  
 PT

PS Claim 3; Col 29-34; 23pp; English.  
 XX This sequence represents the human neuropeptide Y5 receptor (Y5) protein.  
 CC The protein is useful for screening for compounds able to be used as  
 CC agonists and antagonists to the Y5 receptor, especially for the treatment  
 CC obesity and diabetes and for developing antibodies for the detection of  
 CC the protein  
 XX  
 SQ Sequence 445 AA;  
 Alignment Scores:  
 Pred. No.: 1,566-247 Length: 445  
 Score: 2330.00 Matches: 445  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.95% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-771-956-4 (1-1406) x AAY14554 (1-445)  
 QY 47 ATGGATTAGAGCTCGACGAGTATTATAACAAGACACTTGCACAGAGATAATACTGCT 106  
 Db 1 MetAspLeuGluLeuAspGluTrpAsnLysThrLeuAlaThrGluAsnAsnThrAla 20  
 QY 107 GCCACTCGGAATTTCTGATTTCCAGTCTGGGATGACTATAAAGCAGTGCTAGATGACTTA 166  
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTrpLysSerSerValAspAspLeu 40  
 QY 167 CAGTATTTTCTGATGGGCTCTATACATTGTAAAGTCTTTTGGCTTTATGGGGAATCTA 226  
 Db 41 GlnTrpPheLeuLleGlyLeuTrpPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 QY 227 CITATTTTAAATGGCTCTCATGAAAAGCGTATATCAGACACTACGGTAAACTTCTCATA 286  
 Db 61 LeuLleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuLle 80  
 QY 287 GCAATCTCGGCTTTTCTGATATCTTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 346  
 Db 81 GlyAsnLeuAlaPheSerAspLleLeuValValLeuPheCysSerProPheThrLeuThr 100  
 QY 347 TCTGCTCTGCTGATCAGTGGATGTTTGGCAAAAGTCATGTGCCATATATTGCTTTTCTT 406  
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisLleMetProPheLeu 120  
 QY 407 CAATGTGTCTCAGTTTGGTTCACCTTTAAATTTAATATCAATTCACATTTGTCAGGTAT 466  
 Db 121 GlnCysValSerValLeuValSerThrLeuLleLeuLleSerLleAlaLleValArgTrp 140  
 QY 467 CATATGATAAAACATCCCATATCTAATAATTTAAACAGCAAAACCATGGCTACTTTCTGATA 526  
 Db 141 HisMetLleLysHisProLleSerAsnAsnLeuThrAlaAsnHisGlyTrpPheLeuLle 160  
 QY 527 GCTACTGTCTGACACTAGTTTGGCATCTGTTCTCCCTCCCTCCCTCCCTCCCTCCCTCC 586  
 Db 161 AlaThrValTrpThrLeuGlyPheAlaLleCysSerProLeuProValPheHisSerLeu 180  
 QY 587 GTGGAACCTTCAAGAAACATTTGGTTCAGCATTTGTCAGCAGCAGCAGCATTTATGTTGTCAG 646  
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTrpLeuCysValGlu 200  
 QY 647 TCATGGCCATCTGATTCATACAGATTGCTTACTATCTCTTTTACTTCTTCTTCTTCTTCT 706  
 Db 201 SerTrpProSerAspSerTrpArgLleAlaPheThrLleSerLeuLeuValGlnTrp 220  
 QY 707 ATTCTGCCCTTAGTTTGTCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 766  
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerLleSerCys 240  
 QY 767 GGATTTGTCACAAAGAAAGAAACAGACTTGAAGAAATAGATGATCAACTTAACCTTCTCAT 826  
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluAsnGluMetLleAsnLeuThrLeuHis 260  
 QY 827 CCATCAAAAAGAGTGGGCTCAGTGAAACTCTCTGGCAGCCATAAATGGAGTTATTCA 886

Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280  
QY 887 TTTATCAAAACACAGAGAGATATAGCAAGACAGCATGTGTGTACTGCTTCCA 946  
Db 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
QY 947 GAAAGACCTTCTCAAGAGACCACTCCAGAAATCTTCCAGAAACCTTGGCTCTGTAAAG 1006  
Db 301 GLUArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320  
QY 1007 AGTCAGCTCTCTTCATCCAGTAAGTTTCATACACAGGGGTCCTGCTTTGAGATAAAA 1066  
Db 321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340  
QY 1067 CCTGAAGAAATTCAGATGTTGATGATTCAGAGTAAGCGTCTGTTCAAGAAATAAAA 1126  
Db 341 ProGluGluAsnSerAspValHsGluLeuArgValLysArgSerValThrArgIleLys 360  
QY 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTGATATTAGTATTGCTGTAGT 1186  
Db 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuValPheAlaValSer 380  
QY 1187 TGAATGCCATACACCTTTCCATGCTGGTAACTGATTTTAATCACATCTTATTTCAT 1246  
Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspLeuIleSerAsn 400  
QY 1247 AGGCATTTCAAGTGTGTGTTATGCTATTGTCATTTGTTGGCATGATGCTCTGTTCTT 1306  
Db 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLysLeu 420  
QY 1307 AATCCAAATCTATATGGGTTCTTATAATATGGGATTAAGCTGATTTAGTGTCCCTTATA 1366  
Db 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle 440  
QY 1367 CACTGTCTTCATATG 1381  
Db 441 HisCysLeuHisMet 445  
RESULT 15  
ID AAY52578  
XX AA52578 standard; protein; 445 AA.  
XX AA52578;  
XX  
DT 28-FEB-2000 (first entry)  
XX Human NPY (neuropeptide Y) Y5 receptor.  
XX Neuropeptide Y; NPY; receptor; Y5; G-protein coupled; expression;  
KW chimeric; pharmacological property; peripheral nervous system;  
KW central nervous system; physiological; activity; food intake; feeding;  
KW thermogenesis; blood pressure; hormone release; gut motility;  
KW smooth muscle tone; sleep; circadian rhythm; neuronal excitability;  
KW nociception; mood; emotional response; seizure activity; diuresis;  
KW natriuresis; calciuresis; antisenescence; agonist; antagonist; obesity;  
KW hypertension; epilepsy; sexual dysfunction; jet lag.  
XX  
OS Homo sapiens.  
XX  
XX US5985616-A.  
XX  
PD 16-NOV-1999.  
XX  
XX 07-JAN-1998; 98US-00003199.  
XX  
XX 07-JAN-1998; 98US-00003199.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Parker EM, Rudinski MS, Strader CD;  
XX  
XX WPI; 2000-012792/01.  
XX  
DR

DR N-PSDB; AAZ46232.  
XX Chimeric mammalian neuropeptide Y5 receptor polypeptides useful for  
PT treating a range of disorders including jet lag, hypertension and sexual  
PT dysfunction.  
XX  
XX Example; Col 37-40; 24pp; English.  
XX  
XX This sequence represents human neuropeptide Y (NPY) Y5 receptor, cDNA  
CC encoding which was isolated and amplified from a human neuroblastoma cell  
CC line using primers AAZ46215-246223. The receptor was transiently  
CC expressed in COSI cells, but its level of expression was found to be  
CC significantly lower in comparison to that of the rat NPY Y5 receptor  
CC (AA52579). The invention relates to a chimeric rat/human NPY receptor,  
CC comprising the 5' untranslated region (5' UTR) and extreme 5' coding  
CC region (105 bp) of the rat Y5 receptor cDNA, appended to nucleotides 365-  
CC 1633 of the human Y5 receptor cDNA. When transfected into COSI cells, the  
CC chimeric construct yielded levels of expression higher than the native  
CC human Y5 receptor, and similar or greater levels of expression than the  
CC native rat Y5 receptor. The pharmacological properties of the chimeric  
CC receptor were similar to those of the native human Y5 receptor. NPY is  
CC widely distributed in both the peripheral and central nervous systems and  
CC has a wide range of physiological activities including effects on food  
CC intake, thermogenesis, blood pressure, hormone release, gut motility,  
CC smooth muscle tone, sleep and circadian rhythms, neuronal excitability,  
CC nociception, mood and emotional responses. NPY mediates these  
CC physiological effects via interactions with at least six distinct G-  
CC protein coupled receptors (designated Y1-Y6). The Y5 receptor mediates  
CC the effects of NPY on feeding, thermogenesis, neuronal excitability and  
CC seizure activity, diuresis, natriuresis and calciuresis. The chimeric Y5  
CC receptor, associated nucleic acids (e.g., expression vectors or antisense  
CC molecules), agonists or antagonists may be administered to treat  
CC disorders such as obesity, hypertension, epilepsy, sexual dysfunction and  
CC jet lag associated with abnormal expression/activity of NPY  
XX  
XX Sequence 445 AA;  
Alignment Scores:  
Pred. No.: 1,56e-247 Length: 445  
Score: 2330.00 Matches: 445  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.95% Indels: 0  
DB: 3 Gaps: 0  
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Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20  
QY 107 GCCACTCGCAATTCGATTTCCTCCAGTCTCCGATGACTATAAAGCAGCTAGATGACTTA 166  
Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspLeu 40  
QY 167 CAGTATTTCTGATGGGCTCTATACATTGTAAGTCTTCTGGCTTTATGGGAATCTA 226  
Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
QY 227 CTTATTTTATGGCTCTCATGAAAGCGTAATACAGACACTACGCTAACTTCCTCAT 286  
Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuIle 80  
QY 287 GGCAATCTGGCCTTTTCTGATATCTTGGTGTGCTGTTTGTCTCCTTTCACACTGAGC 346  
Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100  
QY 347 TCTGCTCTGCTGATCAGTGATGTTGGCAAGTCATGTCATATTATGCTTTCTT 406  
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120  
QY 407 CAATGTGTGTCAGTGTGTTTCAACTTAAATTAATATCAATTCCTATTCAGGTAT 466

Db 121 GlnCysValSerValLeuValSerThrLeuLeuLeuSerIleAlaIleValArgTyr 140  
QY 467 CATATGATAAAACATCCCATATCTAATAATTAAACAGCAAAACCATGGCTACTTTCTGATA 526  
Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160  
QY 527 GCTACTGCTCGACACTAGGTTTCCCATCTGTTCCCTCCCTCCAGTGTTCACAGTCTT 586  
Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
QY 587 GTGGAACCTCAAGAAACATTTGGTTACGATGTGTGACGACGACGATATTATGTGTTGAG 646  
Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200  
QY 647 TCATGGCCATCTGATTCATACAGAAATGCCCTTACTATCTCTTATTCTAGTTCAGTAT 706  
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QY 707 ATTCTGCCCTTAGTTGCTTACTGTAGTCATACAAAGTGTCTGCAGAAGTATAAGCTGT 766  
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
QY 767 GGATGTCTCAACAGAAACAGACTTGAAGAAATGAGATGATCAACTTAACCTTCAT 826  
Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluAsnGluMetIleAsnLeuThrLeuHis 260  
QY 827 CCATCCAAAAGAGTGGCCCTCAGGTGAACCTCTCTGCCAGCCATAAATGGAGTTATTCA 886  
Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280  
QY 887 TTCATCAAAAACACAGAAAGATATAGCAAGAGACAGCATGTGTGTACCTGTCTCCA 946  
Db 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
QY 947 GAAAGACCTTCTCAAGAGAACCTCCAGAAATACCTCCAGAAACCTTTGGCTCTGTAAGA 1006  
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QY 1007 AGTCAGCTCTCTTCATCCAGTAACTTCATACCGGGTCCCCACTTGCTTTGAGATAAAA 1066  
Db 321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340  
QY 1067 CCTCAAGAAATTCAGATGTTTCATGAATTCGAGTAAACGTTCTGTTCAGAAATAAA 1126  
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QY 1127 AAGAGATCTCGAGTGTGTTTCTACAGACTGCACCATCTGATATTAGTATTGCTGTAGT 1186  
Db 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuValPheAlaValSer 380  
QY 1187 TGGATGCCACTACACCTTTCCATGCTGGTAACGTATTTAATGACATCTTATTTCAAAT 1246  
Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400  
QY 1247 AGGCATTTCAAGTTGGTGTATTGCTATTGTCATTGTTGGCATGATGCTCTGTGCTCTT 1306  
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QY 1307 AATCCAAATCTATAGGGTTTCTTAATAATGGGATTAAGCTGATTTAGTGTCCCTTATA 1366  
Db 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle 440  
QY 1367 CACTGTCTTCATATG 1381  
Db 441 HisCysLeuHisMet 445



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 21, 2004, 11:38:19 ; Search time 57 Seconds

(without alignments)  
4746.694 Million cell updates/sec

Title: US-09-771-956-4

Perfect score: 2480  
Sequence: 1 ttttggttgctgacaagtgt.....attctcaactgtttaccagg 1406

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPRO\_spool\_P/US09771956/runat\_21102004\_103737\_9386/app\_query.fasta\_1.1543  
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THRT SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09771956@cgn 1.1.74 @runat\_21102004\_103737\_9386 -NCPU=3  
-NO.WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID     | Description           |
|------------|-------|-------------|--------|--------|-----------------------|
| 1          | 481.5 | 19.4        | 366    | S71152 | neuropeptide Y/pep    |
| 2          | 481.5 | 19.4        | 384    | A45490 | G protein-coupled     |
| 3          | 480   | 19.4        | 349    | S12863 | neuropeptide Y/pep    |
| 4          | 480   | 19.4        | 382    | B46133 | neuropeptide Y rec    |
| 5          | 480   | 19.4        | 382    | S27388 | neuropeptide Y/pep    |
| 6          | 464.5 | 18.7        | 375    | I39182 | pancreatic polypep    |
| 7          | 463.5 | 18.7        | 375    | G02300 | neuropeptide Y rec    |
| 8          | 458   | 18.5        | 375    | S63685 | neuropeptide Y/pep    |
| 9          | 455.5 | 18.4        | 381    | I39187 | G protein-coupled     |
| 10         | 404   | 16.3        | 370    | I52315 | sulfinilargin recepto |
| 11         | 384   | 15.5        | 584    | JC7809 | cholecystokinin-A     |
| 12         | 377   | 15.2        | 436    | JC5599 | gastric CCK-A rece    |
| 13         | 375   | 15.1        | 427    | S50150 | cholecystokinin re    |
| 14         | 368.5 | 14.9        | 444    | A42685 |                       |

#### ALIGNMENTS

##### RESULT 1

S71152  
neuropeptide Y/peptide YY receptor Y1 - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 27-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S71152; S55924

R;Martens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.

submitted to the EMBL Data Library, November 1993

A;Description: Cloning and sequencing of an neuropeptide Y/peptide YY receptor from Xenop

A;Reference number: S71152

A;Accession: S71152

A;Molecule type: mRNA

A;Residues: 1-366 <MAR>

A;Cross-references: UNIPROT:P34992; EMBL:L25416; NID:G409169; PIDN:AAA49918.1; PID:G4091

R;Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.

Biochim. Biophys. Acta 1261, 439-441, 1995

A;Title: Cloning and sequence analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA f

A;Reference number: S55924; MUID:95260870; PMID:7742373

A;Accession: S55924

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-278, 'T', 280-366 <BLQ>

A;Cross-references: EMBL:L25416; NID:G409169

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Alignment Scores:

|                        |          |               |     |
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| Pred. No.:             | 6.17e-35 | Length:       | 366 |
| Score:                 | 481.50   | Matches:      | 114 |
| Percent Similarity:    | 43.75%   | Conservative: | 75  |
| Best Local Similarity: | 26.39%   | Mismatches:   | 128 |
| Query Match:           | 19.42%   | Indels:       | 115 |
| DB:                    | 2        | Gaps:         | 8   |

US-09-771-956-4 (1-1406) x S71152 (1-366)

Qy 71 TATACAGACACTTGCACAGAGATAATCTGCTGCCACTCGGAATTCGATTTCCTCA 130

|    |       |      |     |   |        |                     |
|----|-------|------|-----|---|--------|---------------------|
| 15 | 367   | 14.8 | 449 | 2 | A41738 | neuropeptide Y rec  |
| 16 | 356   | 14.4 | 428 | 2 | JN0692 | cholecystokinin ty  |
| 17 | 355.5 | 14.3 | 430 | 2 | I51898 | cholecystokinin A   |
| 18 | 351.5 | 14.2 | 447 | 2 | A47430 | gastrin/cholecysto  |
| 19 | 347   | 14.0 | 455 | 2 | T15622 | hypothetical prote  |
| 20 | 343.5 | 13.9 | 453 | 2 | S2817  | gastrin receptor -  |
| 21 | 339.5 | 13.7 | 452 | 2 | JC2459 | gastrin/cholecysto  |
| 22 | 329.5 | 13.3 | 450 | 2 | JQ1614 | cholecystokinin B   |
| 23 | 329.5 | 13.3 | 452 | 2 | A46195 | glucocorticoid-ind  |
| 24 | 320   | 12.9 | 423 | 2 | B40470 | hypothetical prote  |
| 25 | 316.5 | 12.8 | 457 | 2 | T29741 | allatostatin recep  |
| 26 | 309.5 | 12.5 | 423 | 2 | JC7677 | galanin receptor -  |
| 27 | 308.5 | 12.4 | 394 | 2 | JC7209 | hypothetical prote  |
| 28 | 306.5 | 12.4 | 365 | 2 | T20184 | hypothetical prote  |
| 29 | 303   | 12.2 | 399 | 2 | T16277 | neurokinin 2 recep  |
| 30 | 302.5 | 12.2 | 398 | 1 | JQ1059 | neurokinin 2 recep  |
| 31 | 302.5 | 12.2 | 412 | 2 | T22076 | hypothetical prote  |
| 32 | 300   | 12.1 | 443 | 2 | D40470 | glucocorticoid-ind  |
| 33 | 295.5 | 11.9 | 374 | 2 | T19340 | hypothetical prote  |
| 34 | 294   | 11.9 | 349 | 2 | I59336 | gastrin receptor 1  |
| 35 | 293.5 | 11.8 | 390 | 2 | B86694 | protein AC7.1 [imp  |
| 36 | 293   | 11.8 | 391 | 2 | T32714 | hypothetical prote  |
| 37 | 288.5 | 11.6 | 357 | 2 | JC7319 | probable allatosta  |
| 38 | 288.5 | 11.6 | 384 | 2 | A41007 | gastrin-releasing   |
| 39 | 285   | 11.5 | 376 | 2 | T19186 | hypothetical prote  |
| 40 | 285   | 11.5 | 384 | 1 | S05516 | neurokinin 2 recep  |
| 41 | 284   | 11.5 | 519 | 2 | S17783 | tachykinin recepto  |
| 42 | 282.5 | 11.4 | 514 | 2 | D56849 | dopamine receptor - |
| 43 | 281.5 | 11.4 | 384 | 2 | I57957 | neurokinin 2 recep  |
| 44 | 280.5 | 11.3 | 452 | 2 | A34916 | neurokinin 3 recep  |
| 45 | 280.5 | 11.3 | 465 | 1 | JQ1517 | neurokinin 3 recep  |

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Db 6 TyrPheGluAsnLeuSerValProAsnAsnIleSerGly-----AsnIleThrPhePro 23
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Db 24 IleSerGluAspCysAlaLeuProLeuPro-----MetIlePheThrLeuAlaLeuAla 41
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Db 42 TyrGlyAlaValIleIleIleGlyLeuSerGlyAsnLeuAlaLeuIleIleIleLeu 61
QY 248 AAAAGCGTATCAGAAGACTAGCGTAACCTTCCTCATTAGGCAATCTGGCCCTTTTCTGAT 307
Db 62 LysGlnLysGluMetArgAsnValThrAsnIleLeuIleValAsnLeuSerPheSerAsp 81
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Db 82 LeuLeuAlaThrIleMetCysLeuProPheThrLeuIleIleThrLeuMetAspHisTrp 101
QY 368 ARGTTTGGCAAGTCATGTGCCATATTATGCTTTTCTCAATGCTGTGCTGCTGCTGCT 427
Db 102 IlePheGlyGluValMetCysLysLeuAsnGluTyrIleGlnCysValSerValThrVal 121
QY 428 TCAACTTTAATTTAATATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
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QY 488 TCTAATAATTTAACAGCAAAACCATGGCTACTTCTGATAGTACTGCTGCTGCTGCTGCT 547
Db 142 GlyTyrArgProAsnAsnArgHisAlaCysPheGlyIleThrValIleTrpGlyPheAla 161
QY 548 TTGTCATCTGCTTCCCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
Db 162 MetAlaCysSerThrProLeuMetMetTyrSerValLeuThrAsp-----GluProPhe 179
QY 608 GTTTCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658
Db 180 LysAsnIleSerLeuAspSerTyrIleGlyLysTyrValCysLeuGluAspPheProGlu 199
QY 659 GATTCATCAGAAATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 718
Db 200 AspLysPheArgLeuSerThrThrLeuLeuPheIleLeuGlnTyrLeuGlyProLeu 219
QY 719 GTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 778
Db 220 CysPheIlePheValCysTyrThrLysIle----- 229
QY 779 AAAGAAACACAGCTTGAAGAAATGAGATGATCACTTAACTTCTTCTTCTTCTTCTTCTTCT 838
Db 229 ----- 229
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Db 234 LysArg----- 236
QY 959 CAAGAGAACCACTCCAGAACTATCTCCAGAAAACTTGGCTCTGTGAAGATGCTGCTCT 1018
Db 236 ----- 236
QY 1019 TCATCCAGTAGTTTCATACCAGGGGCTCCCACTTCTGCTTTCAGATATAAACTGAAGAAAT 1078
Db 237 -----Asn 237
QY 1079 TCAGATGTTCAATGATTCAGAGTAACAGTTCTGTTACAGAATAAAAAAGAGATCTCGA 1138
Db 238 AsnMetMetAspLysIleArgAspAsnLysTyrArgSerSerGluThrLysArg----- 255
QY 1139 AGTGTCTTCTACAGACTGACCATCTCATATTAGTATTCTGCTTCTGCTGCTGCTGCTGCT 1198

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Db 256 ---IleAsnIleMetLeuLeuSerIleValValGlyPheAlaLeuCysTrpLeuProPhe 274
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QY 1319 TATGGTCTTCTTAATATGCGGATTAAGCTGATTTA 1354
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RESULT 2
A45490
Neuropeptide Y/peptide YY receptor Y1 - human
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45490; A46133; A42773
R:Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
J. Biol. Chem. 268, 6703-6707, 1993
A:Title: Genomic organization, localization, and allelic differences in the gene for the
A:Reference number: A45490; MUID:93203272; PMID:8095935
A:Accession: A45490
A:Molecule type: DNA
A:Residues: 1-384 <HER>
A:Note: sequence extracted from NCBI backbone (NCBI:128005; NCBI:128000)
R:Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A:Title: Cloned human neuropeptide Y receptor couples to two different second messenger
A:Reference number: A46133; MUID:922835184; PMID:1321422
A:Accession: A46133
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-384 <HE2>
A:Note: sequence extracted from NCBI backbone (NCBI:108538)
R:Arhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlested, C.
J. Biol. Chem. 267, 10935-10938, 1992
A:Title: Cloning and functional expression of a human neuropeptide Y/peptide YY receptor
A:Reference number: A42773; MUID:92283782; PMID:1317848
A:Accession: A42773
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-384 <LAR>
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A:Experimental source: fetal brain
A:Note: sequence extracted from NCBI backbone (NCBI:104735; NCBI:104736)
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A:Gene: GDB:NPY1R; NPYR
A:Cross-references: GDB:132643; OMIM:162641
A:Map position: 4q31.3-4q32
C:Superfamily: neurokinin 1 receptor
F:77-103/Domain: transmembrane #status predicted <TM1>
F:118-136/Domain: transmembrane #status predicted <TM2>
F:155-179/Domain: transmembrane #status predicted <TM3>
F:209-232/Domain: transmembrane #status predicted <TM4>
F:261-286/Domain: transmembrane #status predicted <TM5>
F:300-323/Domain: transmembrane #status predicted <TM6>
F:113-198/Disulfide bonds: #status predicted
F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:338/Binding site: palmitate (Cys) (covalent) #status predicted
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Pred. No.: 6.18e-35 Length: 384
Score: 481.50 Matches: 115
Percent Similarity: 43.71% Conservative: 76
Best Local Similarity: 26.32% Mismatches: 129
Query Match: 19.42% Indels: 117
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Db 177 IleLeuThrAsp-----GluProPheGlnAsnValSerLeuAlaAlaPheLysAspLys 194  
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Qy 692 TTGCTAGTTCAAGTATATCTGCCCTTAGTTGTCTTACTTAAGTCATACAAAGTGTCTGC 751  
Db 215 LeuValLeuGlnTyrPheGlyProLeuCysPheIlePheIleCysTyrPheLysIle--- 233  
Qy 752 AGAAGTATAGCTGTGGATTGTCCCAACAAAGAAACAGACTTGAAGAAATGAGATGATC 811  
Db 233 ----- 233  
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Db 246 ----- 246  
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Db 247 -----IleArgAspSerLysTyrArgSerSerGlu----- 256  
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Db 256 ----- 256  
Qy 1112 GTTACAGAAATAAAAGAGATCTCGAAGTGTTCAGACTGTTTCTACAGACTGACCATATGATTA 1171  
Db 257 -----ThrLysArgIleAsnValMetLeuLeuSerIleValVal 269  
Qy 1172 GTATTGTGTTAGTTGGATGCCACTACACCTTTTCCATGTGTGTAACCTGATTTTAAATGAC 1231  
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Qy 1352 TTA 1354  
Db 330 Leu 330  
RESULT 5  
S27388  
neuropeptide Y receptor NPY-1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S27388  
R:Eva, C.; Oberto, A.; Sprengel, R.; Genazzani, E.  
FEBS Lett. 314, 285-288, 1992  
A:Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific ex  
A:Reference number: S27388; MUID:93106169; PMID:1468559  
A:Accession: S27388  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-382 <EVA>  
A:Cross-references: UNIPROT:Q04573; EMBL:Z18280; NID:G53438; PIDN:CAA79157.1; PID:G53439  
C:Superfamily: neurokinin 1 receptor

Alignment Scores:

Pred. No.: 8,41e-35 Length: 382  
Score: 480.00 Matches: 114  
Percent Similarity: 42.86% Conservative: 75  
Best Local Similarity: 25.85% Mismatches: 126  
Query Match: 19.35% Indels: 126  
DB: 2 Gaps: 9  
US-09-771-956-4 (1-1406) x S27388 (1-382)  
Qy 74 AACAGACACTT-----GCCACAGAGATAATACCTGCT-----GCCACTCGGAAT 118  
Db 2 AsnSerThrLeuPheSerLysValGluAsnHisSerIleHisTyrAsnAlaSerGluAsn 21  
Qy 119 TCTGATTTCCCACTGCTGGGATGACTATATAAGCAGCTAGTAGCTTACAGTATTTCTGT 178  
Db 22 SerProLeuAlaPheGluAsn-----AspAspCysHisLeuProLeu 36  
Qy 179 ATGGGCTCTATACATT-----GTAAGTCTTCTGGCTTTATGGG 220  
Db 37 AlaValIlePheThrLeuAlaLeuAlaTyrGlyAlaValIleIleLeuGlyValSerGly 56  
Qy 221 AATCTACTTATTTTATATGCTCTCATGAAAAAGCGTAATCAGAAGACTACGGTAACATTC 280  
Db 57 AsnLeuAlaLeuIleIleIleLeuLysGlnLysGluMetArgAsnValThrAsnIle 76  
Qy 281 CTCATAGGCAATCTGGCCTTTTCTGATATCTTGGTGTGCTGCTTTTCTCACCCTTTCACA 340  
Db 77 LeuIleValAsnLeuSerPheSerAspLeuLeuValAlaValMetCysLeuProPheThr 96  
Qy 341 CTGACCTGCTGCTGCTGGATCAGTGTGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCT 400  
Db 97 PheValTyrThrLeuMetAspHisTyrValPheGlyGluThrMetCysLysLeuAsnPro 116  
Qy 401 TTTCTTCAATGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 460  
Db 117 PheValGlnCysValSerIleThrValSerIlePheSerLeuValLeuIleAlaValGlu 136  
Qy 461 AGTATCATCATGATAAACAATCCATATCTAATAATTTAAACAGCAAAACCATGCTACTTT 520  
Db 137 ArgHisGlnLeuIleIleAsnProArgGlyTyrArgProAsnAsnArgHisAlaTyrIle 156  
Qy 521 CTGATAGTACTGCTGTCGACACTAGGTTTGGCATCTGTTCTCTCCCTTCCAGCTGTTTAC 580  
Db 157 GlyLeuThrValIleThrValLeuAlaValAlaSerSerLeuProPheValIleTyrGln 176  
Qy 581 AGTCTTGTGGAATCTCAAGAACATTTGTTTCCAGCATTCCTGACGAGC-----AGG 631  
Db 177 IleLeuThrAsp-----GluProPheGlnAsnValSerLeuAlaAlaPheLysAspLys 194  
Qy 632 TATTTATGTTGCTGAGTCATGGCCATCTGATTTCATACAGAAATGCGCTTTACTATCTCTTA 691  
Db 195 TyrValCysPheAspLysPheProSerAspSerHisArgLeuSerTyrThrLeuLeu 214  
Qy 692 TTGCTAGTTCAAGTATATCTGCCCTTAGTTGTCTTACTTAAGTCATACAAAGTGTCTGC 751  
Db 215 LeuValLeuGlnTyrPheGlyProLeuCysPheIlePheIleCysTyrPheLysIle--- 233  
Qy 752 AGAAGTATAGCTGTGGATTGTCCCAACAAAGAAACAGACTTGAAGAAATGAGATGATC 811  
Db 233 ----- 233  
Qy 812 AACTTAACCTTCATCCATCCAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCCAT 871  
Db 233 ----- 233  
Qy 872 AAATGGAGTTATTTCATTCATCAAAAACACAGAAAGATATAGCAAGAGACAGCATGT 931  
Db 234 -----TyrIleArgLeuLysArgArgAsnAsnMetMetAspLys----- 246  
Qy 932 GTGTTACCTGCCAGAAAGACTTCTCAAGAGAACCACTTCCAGAACTTCCAGAAAAC 991  
Db 246 ----- 246

QY 992 TTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTTCATACCAGGGGTCCCCACT 1051  
 Db 247 -----IleArgAspSerLysTyrArgSerGlu----- 256  
 QY 1052 TGCCTTTGAGATAAAACCTGAAGAAAATTTCAGATGTTTCATGAATTGAGAGTAAACGTTCT 1111  
 Db 256 ----- 256  
 QY 1112 GTTACAAGATTAATAAGAGATCTCGAAGTGTCTTACAGACTGACCATCTACTGATTA 1171  
 Db 257 -----ThrLysArgIleAsnIleMetLeuLeuSerIleValVal 269  
 QY 1172 GTATTGTCTGTAGTGGTCCATACACCTTTTCCATGTGGTAAGTGAATTTAAATGAC 1231  
 Db 270 AlaPheAlaValCysTyrProLeuThrIlePheAsnThrValPheAspTyrAsnHis 289  
 QY 1232 AATCTATTCAATAGGCAATTCAGTTGGTGTATTCATTTGTTCATTTGGGGCATG 1291  
 Db 290 GlnIleIleAlaThrCysAsnHisAsnLeuLeuPheLeuLeuCysHisLeuThrAlaMet 309  
 QY 1292 ATGTCCTGTGTCTTAATCCCAATCTATATGGGTTTCTTAATAATGGGATTAAGCTGAT 1351  
 Db 310 IleSerThrCysValAsnProIlePheTyrGlyPheLeuAsnLysAsnPheGlnArgAsp 329  
 QY 1352 TTA 1354  
 Db 330 Leu 330  
 RESULT 6  
 139182  
 neurotensin Y-peptide YY receptor Y4 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
 C:Accession: I39182  
 R:Barclay, J.A.; Walker, M.W.; Branchek, T.A.; Weinshank, R.L.  
 J. Biol. Chem. 270, 26762-26765, 1995  
 A:Title: Cloning and functional expression of a human Y4 subtype receptor for pancreatic  
 A:Reference number: I39182; MUID:96070761; PMID:7592911  
 A:Accession: I39182  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-375 <RES>  
 C:Cross-references: UNIPROT:P50391; EMBL:U55232; NID:gl063629; PIDN:AAC50280.1; PID:gl06  
 C:Superfamily: neurokinin 1 receptor  
 C:Keywords: appetite

Alignment Scores:  
 Pred. No.: 2,05e-33 Length: 375  
 Score: 464.50 Matches: 102  
 Percent Similarity: 42.86% Conservative: 72  
 Best Local Similarity: 25.12% Mismatches: 121  
 Query Match: 18.73% Indels: 111  
 DB: 2 Gaps: 6  
 US-09-771-956-4 (1-1406) x I39182 (1-375)

QY 161 GACATACAGTATTTCTGATGGGCTCTATACATTTCTAGTCTTCTTGGCTTTATGGG 220  
 Db 39 AspValMetValPheIleValThrSerTyrSerIleGluThrValValGlyValLeuGly 58  
 QY 221 AATCTACTATTATTAATGGCTCTCATGAAGAGCGTAATCAGAGACTACGGTAAACCTC 280  
 Db 59 AsnLeuLeuMetCysValThrValArgGlnLysGluLysAlaAsnValThrAsnLeu 78  
 QY 281 CTCATAGCAATCTGGCTTTCTGATATCTGGTGTGGTCTTCTTCTCCTCCTTTCACA 340  
 Db 79 LeuIleAlaAsnLeuAlaPheSerAspPheLeuMetCysLeuLeuCysGlnProLeuThr 98  
 QY 341 CTGACGTCTGTCTGGTGGATGATGTTTGGCAAGATCATGTGCCATATATATGCT 400  
 Db 99 AlaValTyrThrIleMetAspTyrTyrIlePheGlyGluThrLeuLeuCysLysMetSerAla 118  
 QY 401 TTTCTCAATGTGTCTGCTGTTGGTTCACATTTTAATATATCAATGCCATGTC 460

Db 119 PheIleGlnCysMetSerValThrValSerIleLeuSerLeuValValAlaLeuGlu 138  
 QY 461 AGGTATCATATGATAAAACATCCCATATCTAATAATTTAAACAGCAAAACCATGGCTCTTT 520  
 Db 139 ArgHisGlnLeuIleAsnProThrGlyTyrLysProSerIleSerGlnAlaTyrLeu 158  
 QY 521 CTGATAGTACTGTCTGGACACTAGTGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 580  
 Db 159 GlyIleValLeuIleThrValIleAlaCysValLeuSerLeuProphe---LeuAlaAsn 177  
 QY 581 AGTCTTGTGGAA-----CTTCAAGAAACATTTGGTTCAGCAATG-----CTGAGCAGC 628  
 Db 178 SerIleLeuGluAsnValPheHisLysAsnHisSerLysAlaLeuGluPheLeuAlaAsp 197  
 QY 629 AGGTATTTATGTGTGAGTCATGGCCATCTGATTCATACAGAAATTCCTTTACTTCTCT 688  
 Db 198 LysValValCysThrGluSerThrProLeuAlaHisHisArgThrIleTyrThrThrPhe 217  
 QY 689 TTATTCTAGTTTCTGATATATCTGCTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 748  
 Db 218 LeuLeuLeuPheGlnTyrCysLeuProLeuGlyPheIleLeuValCysTyrAlaArgIle 237  
 QY 749 TGCAGAAAGTATAAGCTGTGGATTGCTCAACAAAGAAACAGACTTGAAGAAAATGAGATG 808  
 Db 238 TyrArg-----ArgLeuGlnArgGlnGlyArg 246  
 QY 809 ATCAACTTAACCTTCTTCATCCATCCAAAGAGTGGGCTCAGGTGAAACTCTCTGGCAGC 868  
 Db 247 Val-----Phe 248  
 QY 869 CATAAATGAGTATTTATTCATTCATCAAAACACACAGAAAGATATAGCAAGAACAGACA 928  
 Db 249 HisLysGlyThrTyrSerLeuArgAlaGlyHisMetLysGln----- 262  
 QY 929 TGTGTGTTACTCTGCTCCAGAAAGACCTCTTCAAGAGAACCTCCTCCAGAAATATCTCCAGAA 988  
 Db 262 ----- 262  
 QY 989 AACTTTGGCTCTGTAAAGTACAGCTCTTTCATCCAGTAAGTTTCATACCAGGGTCCCC 1048  
 Db 262 ----- 262  
 QY 1049 ACTTGCTTTGAGATAAAACCTGAAGAAAATTCAGATGTTTCATGATTCAGAGTAAACGT 1108  
 Db 262 ----- 262  
 QY 1109 TCTGTTTACAAGATAAAAGAGATCTCGAAGTGTGTTTCTACAGACTGACCATCTGATA 1168  
 Db 263 -----ValAsnValValLeuValValMetVal 271  
 QY 1169 TTAGTATTTGCTGTAGTTGATGCCACTACACCTTTCCATGCTGGTGAATTAAT 1228  
 Db 272 ValAlaPheAlaValLeuThrProLeuHisValPheAsnSerLeuGluAspThrHis 291  
 QY 1229 GACAATCTTATTCAATAGGCAATTCAGTTGGTGTATTCATTTGCTTCTTGTGGC 1288  
 Db 292 HisGluAlaIleProIleCysHisGlyAsnLeuIlePheLeuValCysHisLeuAla 311  
 QY 1289 ATGATGCTCTGTGTCTTAACTCAATTCATATGGGTTTCTTAATATGGGATTAACCT 1348  
 Db 312 MetAlaSerThrCysValAsnProPheIleTyrGlyPheLeuAsnThrAsnPhelLys 331  
 QY 1349 GATTTAGTGTCCCTTATA 1366  
 Db 332 GluIleLysAlaLeuVal 337

RESULT 7  
 G02300  
 pancreatic polypeptide receptor - human  
 C:Species: Homo sapiens (man)  
 C>Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
 C:Accession: G02300

R.Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.  
submitted to the EMBL data Library, December 1995  
A.Reference number: H01018  
A.Accession: G02300  
A.Accession: G02300  
A.Status: preliminary; translated from GB/EMBL/DDDJ  
A.Molecule type: mRNA  
A.Residues: 1-375 <YAN>  
A.Cross-references: UNIPROT:P50391; EMBL:U42387; PIDN:AA807759.1; PID:IG  
C.Superfamily: neurokinin 1 receptor

| Alignment Scores:      |          |
|------------------------|----------|
| Pred. No.:             | 2,52e-33 |
| Score:                 | 463.50   |
| Length:                | 375      |
| Matches:               | 102      |
| Conservative:          | 72       |
| Best Local Similarity: | 42.86%   |
| Mismatches:            | 121      |
| Query Match:           | 15.12%   |
| Indels:                | 111      |
| DB:                    | 18.69%   |
| Gaps:                  | 2        |
|                        | 6        |

US-09-771-956-4 (1-1406) x G02300 (1-375)

**QY** 161 GACTTACAGATTTTCGATTGGCTCTATACATTGTGAAGTCTTCTCGCTTTATGGG 220  
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**Db** 39 AspValMetValPheIleValThrSerTrvSeriIeGLuThrValValGIvalLeuGly 58

QY 221 AATCTACTTATTTTTAATGGCTCTCATGAAAAAGCGTAATCAGAAGACTACGGTAAACTTC 280  
||||| : : : : : : : : : : : : : : :  
Db 59 AsnLeuCysLeuMetCysValThrValArqGlnIvsGIutVsAlaAsnValThrAsnLeu 78

QY 281 CTCATAGGCAATCTGGCCTTTTCTTGATCTCTGGTTGCTGTTTGGCTACCTTTCACA 340  
Db 79 Leu18AlaAsnLeuAlaPheSerAspPheLeuMetCysLeuLeuCysGlnProLeuThr 98

[illegible]

401 TTTCTCAATGTTGTCTAGTTTGGTTTCACCTTTAAATTTTAATCATATTGCCATTGC 460  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
119 PheIteGInCvSmetSerValThrValSerIleLeuSenSerLeuValLeuValAlaLeuGlu 138

QY 461 AGGTATCATATGATAAACAATCCCATATCTATAATTAAACAGCAACCATGGTACTTT 520  
|||::: |||::: |||::: |||::: |||::: |||:::  
Db 139 ArqHisGlnleuilelleAsnProThrGLVTrpLvsProSerIeserGlnAtvrlen 158

521 CTGATAGCTACTGTCTCGACACATAGGTTTGGCATCTGTCTCCCTTCCAGTGTTTCAC 580  
 159 GLVLeValLeuIleLeuValIleAlaCysValLeuSerLeuProPhe--LeuAlaAsp 177

QY 581 AGTCTTGCGAA-----CTTCAAGAACATTGGTTGAGCATTC-----CTGAGCAGC 628  
|||:::|||||:::|||||  
Db 178 SerTfLeuGIuAsnValPheHisTiyAsnHisSerIySAAlcLeuGIuPheLeuAlaASP 197

629 AGGTATTATGTTAGTTCATGGCCATCTGATTCACAGAATTGCCTTACTATCTCT 688  
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198 IvsValValCysThrGlnSerTrpProLeuAlaHisAcrnThrIleGlyThrThrDhe 217

689 TTATTGCTAGTTCAGTATATTCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAAGTGC 748  
218 LeuLeuLeuPheGlnTyrCysLeuProLeuGlyPheLeuValCysTyrAlaArgTle 237

[illegible]

809 ATCAACTTAACCTCTTCATCCATCCAAAAAGATGGGCCTCAGGTGAACCTCTCTGGCAGC 868

**QY** 869 CATAAATGGAGTTATTTCATTCATCAAAAACACAGAGAAGATATAGCAAGACAGCA 928  
||||| :||| ||| :|||  
**b** 249 NISTVGCUMHVSXIAKALGCLWIMetiveCIN----- 252

929 TGTGTGTACCTGCTCCAGAAAGACCTTCTCAAGAGAAACCACTCCAGAATACTTCCAGAA 988

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262 ----- 262
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Db ----- 262
QY TCTGTTCAAGAATAAAAAAGAGATCTCGAAGTGTTTTCTACAGACTGACCATACTGATA 1168
Db ----- 263
ValAsnValValLeuValValMetVal 271
1169 TTAGTATTGCTGTTAGTTGGATGCCACTACACCTTTTCCATGTGTAAGTCACTGATTTTAAAT 1228
QY ::::: ::::: ::::: ::::: ::::: :::::
272 ValAlaPheAlaValLeuIrpLeuPheAsnSerLeuGluAspIrpAsis 291
Db ::::: ::::: ::::: ::::: ::::: :::::
1229 GACAATCTTATTTCAAATAGGCATTTCAAAGTTGGTGTTATTCGATTTGTTCATTTGTGGC 1288
QY ::::: ::::: ::::: ::::: ::::: :::::
292 HisGluAlaIleProIleCysHisGlyAsnLeuIlePheLeuValCysHisLeuLeuAla 311
Db ::::: ::::: ::::: ::::: ::::: :::::
1289 ATGATGTCCTGTTGCTTTAATCAAAATCTATATGGTTTCTTAAATAATGGGATTAAAGCT 1348
QY ::::: ::::: ::::: ::::: ::::: :::::
312 MetAlaSerThrCysValAsnProPheIleTyGlyPheLeuAsnThrAsnPhelysLys 331
Db ::::: ::::: ::::: ::::: ::::: :::::
1349 GATTAGTGTCCCTTATA 1366
QY ::::: ::::: :::::
332 GluIleLysAlaLeuVal 337
Db ::::: ::::: :::::
RESULT 8
S63685
neuropeptide Y receptor D type - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S63685
R:R:Gregor, P.; Millham, M.L.; Feng, Y.; DeCarr, L.B.; McCaleb, M.L.; Cornfield,
FBBS Lett. 381, 58-62, 1996
A:Title: Cloning and characterization of a novel receptor to pancreatic polypep-
A:Reference number: S63685; MUID:96193913; PMID:8641440
A:Accession: S63685
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-375 >GRE>
A:Cross-references: UNIPROT:Q61041; EMBL:U40189; NID:gi232969; PIDN:AACS2442.1;
C:Superfamily: neurokinin 1 receptor

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| Alignment Scores:      |          |
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| Pred. No.:             | 7.83e-33 |
| Score:                 | 458.00   |
| Length:                | 375      |
| Matches:               | 105      |
| Conservative:          | 65       |
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| Best Local Similarity: | 25.12%   |
| Query Match:           | 18.47%   |
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| Gaps:                  | 7        |
| Indels:                | 138      |
| Mismatches:            | 120      |
| Conservative:          | 65       |
| Matches:               | 105      |
| Length:                | 375      |

US-09-771-956-4 (1-1406) x S63685 (1-375)

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| 161 | QY | GACTACAGTATTCTCGATTGGCTCTCATCATTTGAAGTCCTCTTGGCTTTATGGG      | 220 |
| 39  | Db | GlueLeuAlaPheIleIleThrThrTySerIleGluThrIleuGlyValIeuGly      | 58  |
| 221 | QY | AATCTACTTTATTTAATGGCTCTCATGAAAAAGCGTAATCAAGACACTACGGTAAACCTC | 280 |
| 59  | Db | AsnLeuCysLeuIlePheValThrThrArgGlnLysGluLysSerAsnValThrAsnLeu | 78  |
| 281 | QY | CTCATAGGCAATCTGGCTTTCTGATATCTGGTTGTGCTGTTTGTCTCACTTTCACA     | 340 |
| 79  | Db | LeuIleAlaAsnLeuAlaPheSerAppPheLeuMetCysLeuIleCysGlnProLeuThr | 98  |
| 341 | QY | CTGACGCTCTCTGTGTCATCAGTGGATGTGTTGGCAAGTCATGTCGCATATTATGGCT   | 400 |
| 99  | Db | ValThrTyThrIleMetAspTyTrpIlePheGlyGluValIleCysLysMetLeuThr   | 118 |

QY 401 TTCTTCAATGTGTGTCAGTGGTTTCACTTTAAATTTAAATCAATGCGCATTC 460  
 Db 119 PheileGlnCysMetSerValThrValSerLeuValLeuValAlaLeuGlu 138  
 QY 461 AGTATCATATGATAAACAATCCATATCTAATATTTAAACAGAAACCATGCGTACTTT 520  
 Db 139 ArgHisGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 158  
 QY 521 CTGATAGTACTGTCTGGACACTAGGTTTGGCCATCTGTCTCCCTCTT----- 568  
 Db 159 GlyIleValValIleTrpPheileSerCysPheLeuSerLeuProPheLeuAlaAsnSer 178  
 QY 569 -----CCAGTGTTCAC-----AGTCTGTGGAACTTCAGAAACATTT 607  
 Db 179 ThrLeuAsnAspLeuPheHisTyrAsnHisSerLysValValGlu----- 193  
 QY 608 GGTTCAGCATTCCTGAGCAGCAGGATTTATGTGTGATGTCATGCCATCTCATATC 667  
 Db 194 -----PheLeuGluAspLysValValCysPheValSerTrpSerAspHisHis 210  
 QY 668 AGAATGCTTTACTATCTCTTTATGCTAGTGTAGTATATTCGCCCTTGTGTGCTT 727  
 Db 211 ArgLeuIleTyrThrPheLeuLeuLeuPheGlnTyrCysIleProLeuAlaPheile 230  
 QY 728 ACTGTAAGTACATCAAGTGTCTGTCAGAAAGTATAGCTGTGGATGTCACCAAGAAAC 787  
 Db 231 LeuValCysTyrIleArgIleTyrGlnArgLeu----- 241  
 QY 788 AGACTTGAAGAAATGAGATGATCAACTTAATCTTTCATCCATCAAAAGAGTGGCCT 847  
 Db 241 ----- 241  
 QY 848 CAGGTGAAACTCTCTGGCGCCATAAATGGAGTTATTCAATTCATCAAAACACAGAGA 907  
 Db 241 ----- 241  
 QY 908 AGATATAGCAAGACAGCATGTGTGTACCTGCTCAGAAAGACCTTCTCAAGAGAAC 967  
 Db 242 -----GlnArgGlnLysHisValPhe 248  
 QY 968 CACTCCAGAACTTCCAGAAACCTTGGCTCTGTAGAGAGTGTCTCTTATCCAGT 1027  
 Db 249 HisAlaHisAlaCysSerSerArgAlaGlyGlnMet----- 260  
 QY 1028 AAGTTTATACCAGGGGTCCCACTTGTCTTGTAGATAAAACCTGAAGAAATTCAGATGTT 1087  
 Db 260 ----- 260  
 QY 1088 CATGAATGAGAGTAAACAGTCTGTACAGAAATAAAGAGATCTCGAAGTGTTC 1147  
 Db 261 -----LysArgIleAsnSerMet--- 266  
 QY 1148 TACAGACTGACCACTGATATATAGTATTGCTGTGTAGTGGATGCCACTACACCTTTTC 1207  
 Db 267 -----LeuMetThrMetValThrAlaPheAlaValLeuTrpLeuProLeuHisValPhe 284  
 QY 1208 CATGTGTAACTGATTTAATAGCAATCTTATTTCAATAGGCAATTCAGTGTGTAT 1267  
 Db 285 AsnThrLeuGluAspTrpTyrGlnGluAlaIleProAlaCysHisGlyAsnLeuIlePhe 304  
 QY 1268 TGCATTTGTGATTTGTTGGCATGATCTGCTGTGTCTTAAATCAATTCATATGCTGTT 1327  
 Db 305 LeuMetCysHisLeuLeuAlaMetAlaSerThrCysValAsnProPheIleTyrGlyPhe 324  
 QY 1328 CTTAATATGGGATTAAGCTGATTTAGTGTCCCTTATA-----CACTGT 1372  
 Db 325 LeuAsnIleAsnPheLysLysAspIleLysAlaLeuValLeuThrCysHisCys 342

RESULT 9

neuropeptide Y/peptide YY receptor Y2 - human

N;Alternate names: neuropeptide Y/peptide YY receptor type 2

C;Species: Homo sapiens (man)  
 C;Date: 01-Mar-1996 #sequence revision 01-Mar-1996 #text\_change 09-Jul-2004  
 C;Accession: I39187; I39163; G02301  
 R;Gerald, C.; Walker, M.W.; Vayssie, P.J.  
 J. Biol. Chem. 270, 26758-26761, 1995  
 A;Title: Expression cloning and pharmacological characterization of a human hippocampal  
 A;Reference number: I39187; MUID:96070760; PMID:7592910  
 A;Accession: I39187  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-381 <GER>  
 A;Cross-references: UNIPROT:P49146; EMBL:U36269; NID:G1063633; PIDN:AAC50281.1; PID:G1063  
 R;Rose, P.M.; Fernandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kier  
 J. Biol. Chem. 270, 22661-22664, 1995  
 A;Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptide  
 A;Reference number: I39163; MUID:96032678; PMID:7559383  
 A;Accession: I39163  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-133, 'A', 135-381 <ROS>  
 A;Cross-references: EMBL:U32500; NID:G1000750; PIDN:AAA93170.1; PID:G1000751  
 R;Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.  
 Submitted to the EMBL Data Library, December 1995  
 A;Reference number: H01019  
 A;Accession: G02301  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-171, 'G', 173, 'R', 175-201, 'P', 203-208, 'A', 210-381 <YAN>  
 A;Cross-references: EMBL:U42389; NID:G1314329; PIDN:AAB0760.1; PID:G1314330  
 C;Genetics:  
 A;Gene: GDB:NPY2R  
 A;Cross-references: GDB:4365607; OMIM:162642  
 A;Map position: 4q31-4q31  
 C;Superfamily: neurokinin 1 receptor  
 C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester  
 F;49-76/Domain: transmembrane #status predicted <TM1>  
 F;87-113/Domain: transmembrane #status predicted <TM2>  
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 F;221-237/Domain: transmembrane #status predicted <TM5>  
 F;269-291/Domain: transmembrane #status predicted <TM6>  
 F;305-328/Domain: transmembrane #status predicted <TM7>  
 F;123-203/Disulfide bonds: #status predicted  
 F;342/Binding site: palmitate (Cys) (covalent) #status predicted  
 F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
 Pred. No.: 1,31e-32 Length: 381  
 Score: 455.50 Matches: 104  
 Percent Similarity: 43.03% Conservative: 72  
 Best Local Similarity: 25.43% Mismatches: 114  
 Query Match: 18.37% Indels: 119  
 DB: 2 Gaps: 9

US-09-771-956-4 (1-1406) x I39187 (1-381)

QY 161 GACTTACAGTATTTCTGATGGGCTCTATACATTTGTAGCTCTTCTGGTATATGGG 220  
 Db 48 GluValGlnValValLeuIleLeuAlaTyrCysSerIleLeuLeuGlyValIleGly 67  
 QY 221 AATCTACTATTTTAAATGGCTCTCATGAAAGCGTAAATCAGAGACTACGGTAAATTC 280  
 Db 68 AsnSerLeuValIleHisValIleLysPheLysSerMetArgThrValThrAspPhe 87  
 QY 281 CTCATAGCAATCGGCTTTCTCATATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 340  
 Db 88 PheIleAlaAsnLeuAlaValAlaAspLeuValAsnThrLeuCysLeuProPheThr 107  
 QY 341 CTGAGCTGTCTTCTGCGGATCAGTGGATGTTTGGCAAGTCATGTCATATATGCT 400  
 Db 108 LeuThrTyrThrLeuMetGlyGluTrpLysMetGlyProValLeuCysHisLeuValPro 127  
 QY 401 TTTCTTCAATGTGTGTCAGTGTTCAGTTTTCAGTTTAAATTTTAAATATCAATTCGCAATGTC 460  
 Db 401 TTTCTTCAATGTGTGTCAGTGTTCAGTTTTCAGTTTAAATTTTAAATATCAATTCGCAATGTC 460



Db 128 TyrAlaGlnGlyLeuAlaValGlnValSerThrIleThrLeuThrValIleAlaLeuAsp 147  
Qy 461 AGTATCATATGATAAATCATCCATATCTAATAATTAACAGCAACCATGCTACTTT 520  
Db 148 ArgHisArgCysIleValTyrHisLeuGluSerLysIleSerLysArgIleSerPheLeu 167  
Qy 521 CTGATAGCTACTGCTCGACACTAGGTTTGGCCATCTGTTCTCCCTTCCAGTGT--- 577  
Db 168 IleIleGlyLeuAlaTrpGlyIleSerAlaLeuLeuAlaSerProLeuAlaIlePheArg 187  
Qy 578 ---CACAGTCTTGGAACCTCAAGAAACATTTGGTTCCAGATTGCTGACAGCAGGTAT 634  
Db 188 GluTyrSerLeuIleGluIleIleProAspPhe-----GluIleVal 201  
Qy 635 TTATGTTGTCAGTCATCGGCATCTGATTCA-----TACAGAAATGCTTTACTATC 685  
Db 202 AlaCysThrGluLysTrpProGlyGluGlySerIleTyrGlyThrValTyrSerLeu 221  
Qy 686 TCTTTATTGCTAGTATGATTAATCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAGT 745  
Db 222 SerSerLeuLeuIleLeuTyrValLeuProLeuGlyIleIleSerPheSerTyrThrArg 241  
Qy 746 GTCGACAGATATAAGCTGTGGATTGTCCACAAAGAACACAGACTTGAAGAAATGAG 805  
Db 242 Ile----- 242  
Qy 806 ATGATCAACTTAACCTTTCATCCATCCAAAGAGTGGGCTCAGGTGAAACTCTCTGGC 865  
Db 242 ----- 242  
Qy 866 AGCCATAAATCGAGTTATTCTATTCATCAAAACACACAGAGATATAGCAGAGACA 925  
Db 243 -----TrpSer----- 244  
Qy 926 GCATGTGTGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGATACTTCCA 985  
Db 245 -----LysLeuLysAsnHis----- 249  
Qy 986 GAAAACTTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAAGTTCATACAGGGGTC 1045  
Db 250 -----ValSerProGlyAla 254  
Qy 1046 CCCACTGCTTTGAGATAAAACCTGAGAAATTCAGATGTTTCATGAATTCAGAGTAAAA 1105  
Db 255 -----AlaAsnAspHisTyrHisGlnArgArgGlnLys 265  
Qy 1106 GCTTCTGTTCAAGAATAAAAGAGATCTCGAAGTGTCTTCTACAGACTGACCATACTG 1165  
Db 266 -----ThrThrLysMet-----LeuValCysVal 273  
Qy 1166 ATATTAGTATTGCTGTGTTAGTGGATGCCACTACACCTTTTCCATGCTGCTAAGTATT 1225  
Db 274 ValValValPheAlaValSerTrpLeuProLeuHisAlaPheGlnLeuAlaValAspIle 293  
Qy 1226 AATGACAATCTTATTTCAAATAGGCATTTCAAGTTGGTGTATTGATTTGCTATTGTTG 1285  
Db 294 AspSerGlnValLeuAspLeuLysGluTyrLysLeuIlePheThrValPheHisIleIle 313  
Qy 1286 GGCATGATGCTGTGTTTATCAATTCATATGCTTATGCTTCTTATTAATAGGATTA 1345  
Db 314 AlaMetCysSerThrPheAlaAsnProLeuLeuTyrGlyTrpMetAsnSerAsnTyrArg 333  
Qy 1346 GCTGATTAGTGTCCCTTATACACTGT 1372  
Db 334 LysAlaPheLeuSerAlaPheArgCys 342

RESULT 10  
152315  
G protein-coupled receptor UHR-1 - rat  
C:Species: Rattus sp. (rat)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 19-May-2000  
C:Accession: 152315  
R:Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.

Biochem. Biophys. Res. Commun. 209, 606-613, 1995  
A:Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from :  
A:Reference number: 152315; MUID:95251659; PMID:773930  
A:Accession: 152315  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-370 <RES>  
A:Cross-references: GB:S77867; NID:g998527; PIDN:AAB34129.1; PID:g998528  
C:Superfamily: neurokinin 1 receptor

Alignment Scores:  
Pred. No.: 5,338-28 Length: 370  
Score: 404.00 Matches: 111  
Percent Similarity: 41.07% Conservative: 66  
Best Local Similarity: 25.75% Mismatches: 138  
Query Match: 16.29% Indels: 116  
DB: 1 Gaps: 9

US-09-771-956-4 (1-1406) x 152315 (1-370)  
Qy 86 GCCACAGAGATAATACTCTGCTCCACCTCGGAATTCGATTCCCGAGTCTGGAGTACTAT 145  
Db 32 AlaSerGluSerAsnValSerAlaThrValPProAlaAlaVal---ThrProPhe 50  
Qy 146 AAAAGC-----AGTCTAGATGACTTACAGTATTTCTGATTGGGCTCTATACATTTGTA 199  
Db 51 GlnSerLeuGlnLeuValHisGlnLeuLysGlyLeuIleValMetLeuTyrSerIleVal 70  
Qy 200 AGTCTTCTTGGTCTTATGGGAATCTACTATTATTTAAATGGCTCTCATGAAAGCGTAAT 259  
Db 71 ValValValGlyLeuValGlyAsnCysLeuLeuValLeuValIleAlaArgValArg 90  
Qy 260 CAGAACTACGCTAACTTCTCATAGCAATCTGGCCTTTCTGATATCTGTTGTTG 319  
Db 91 LeuHisAsnValThrAsnPheLeuIleGlyAsnLeuAlaLeuSerAspValLeuMetCys 110  
Qy 320 CTGTTTGTCTACCTTTTCACTTCACTGACGTCTGCTTGTGGATCAG---TGGATGTTGGC 376  
Db 111 AlaAlaCysValProLeuThrLeuAlaTyrAlaPheGluProArgGlyTrpValPheGly 130  
Qy 377 AAAGTCATGTCATATTATGCTTTTCTTAATGTGTCTGATGTTGTTGTTCAACTTTA 436  
Db 131 GlyGlyLeuCysHisLeuValPhePheLeuGlnProValThrValTyrValSerValPhe 150  
Qy 437 ATTTTAATCATCTCCATGTCAGTATCATATAAATCATCCCATCTATAAT 496  
Db 151 ThrLeuThrThrIleAlaValAspArgTyrValValLeuValHisProLeuArgArg 170  
Qy 497 TTAACAGCAAAACCATGGCTACTTTCTGATAGTACTGTCTGGACACTAGTGTTCATC 556  
Db 171 IleSerLeuLysLeuSerAlaTyrAlaValLeuGlyIleTrpAlaLeuSerAlaValLeu 190  
Qy 557 TGTCTCCCTCCAGTGTTCACAGTCTGTGGAACTTCAAGAAACATTTGTTTCAGCA 616  
Db 191 AlaLeuProAlaAlaValHisThrTyrHisValGluLeuLysPro----- 205  
Qy 617 TTGCTGAGCAGCAGGATTTTATGTTGTAGTCTATGCCCCTCT---GATTTCATACAGAA 673  
Db 206 -----HisAspValArgLeuCysGluGluPheTrpGlySerGlnArgGlnArgGln 223  
Qy 674 GCOTTTACTATCTCTTTTATGCTAGTTCAGTATATTCTGCCCTTAGTTGCTTACTGTA 733  
Db 224 IleTyrAlaTrpGlyLeuLeuLeuGlyThrTyrLeuLeuProLeuLeuAlaIleLeuLeu 243  
Qy 734 AGTCATACAGTGTCTGCAGAGTATAAGTGTGGATTGTCCCAACAAAGAAACAGACTT 793  
Db 244 SerTyrValArgVal----- 248  
Qy 794 GAAGAAATGAGATGATCAACTTAACCTTTCATCCATCCAAAGAGTGGGCTCAGGTG 853  
Db 249 ----- 250  
Qy 854 AAATCTCTGCGACCCATAAATGGAGTTATTCATTTCATCAAAACAAACAGAGATAT 913

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Db      251 LysLeu-----||||||-----ArgAsnArg--- 255
QY      914 ACAAGAAGACAGCATGTGTACTCTGCTCCAGAAAGACCTTCTCAAGAGAACACCTCC 973
Db      256 -----ValValProGlySerValThrGlnSerGlnAlaAspTrpAsp 269
QY      974 AGAATACTTCCAGAAAACTTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTC 1033
Db      270 Arg-----|||----- 270
QY      1034 ATACCAGGGTCCCACTTGCTTTGAGATAAACCTGAAGAAATTCAGATGTTTCATGAA 1093
Db      270 ----- 270
QY      1094 TTGAGAGTAAACGGTCTCTTACAGAATAAAAAAGAGATCTCGAAGTGTTCCTACAGA 1153
Db      271 -----AlaArgArgArgArgThrPheCysLeu 279
QY      1154 CTGACCATCTGATATTAGTATTGCTGTAGTGGATGCCACATACACCTTTTCCATGTG 1213
Db      280 LeuValValValValValPheAlaLeuCysTrpLeuProLeuHisIlePheAsnLeu 299
QY      1214 GTAACGTATTAAAGACAACTTATTCAATAGGCAATTTCAAGTTGGTGTATTGCAATT 1273
Db      300 LeuArgAspLeuAspProArgAlaIleAspProtyrAlaPheGlyLeuValGlnLeu 319
QY      1274 TGTCAATTTGTTGGCATGATGTCCTGTTGCTTAAATCAATCTATATGAGTGGTTCCTTAAT 1333
Db      320 CysHisTrpLeuAlaMetSerSerAlaCysTyrosinPropheIleTyrAlaTrpLeuHis 339
QY      1334 AATGGATTAAAGCTGATTAGTGTCCCTTATA 1366
Db      340 AspSerPheArgGluGluLeuArgLysMetLeu 350

RESULT 11
JC7809
sulfakinin receptor protein, DSK-R1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C:Accession: JC7809
R:Kubisiak, T.M.; Larsen, M.J.; Burton, K.J.; Bannow, C.A.; Martin, R.A.; Zantello, M.R.;
Biochem. Biophys. Res. Commun. 291, 313-320, 2002
A:Title: Cloning and functional expression of the first Drosophila melanogaster sulfakinin
A:Reference number: JC7809; PMID:11846406; M0ID:21835488
A:Accession: JC7809
A:Molecule type: mRNA
A:Residues: 1-584 <KUB>
C:Cross-references: UNIPROT:Q7M3J6; GB:AX128640
C:Comment: This receptor, the first functionally active orphan Drosophila sulfakinin G-P
actions
C:Genetics:
A:Gene: dsk-r1
A:Map position: 17
F:115-139/Domain: transmembrane region #status predicted <TM1>
F:149-167/Domain: transmembrane region #status predicted <TM2>
F:189-207/Domain: transmembrane region #status predicted <TM3>
F:229-250/Domain: transmembrane region #status predicted <TM4>
F:275-300/Domain: transmembrane region #status predicted <TM5>
F:431-454/Domain: transmembrane region #status predicted <TM6>
F:467-491/Domain: transmembrane region #status predicted <TM7>

Alignment Scores:
Pred. No.: 3.35e-26 Length: 584
Score: 384.00 Matches: 119
Percent Similarity: 41.15% Conservative: 81
Best Local Similarity: 24.49% Mismatches: 186
Query Match: 15.48% Indels: 100
DB: 2 Gaps: 15

US-09-771-956-4 (1-1406) x JC7809 (1-584)
QY      35 CAGGACTATATATGAGTTTACAGCTCCAGCAGTATTATACAGAG-----ACACTT 85

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Db      69 ArgAspGlyTyrrMetAspThrGluProSerAspLeuValThrGluLeuAlaPheSerLeu 88
QY      86 GCCACAGAGAAATAT-----ACTGCTGCCCACTCGGAATTC 121
Db      89 GlyThrSerSerSerProSerProSerThrProAlaSerSerSerThrThrThr 108
QY      122 GATTTCCTCCAGTCTGGGATGACATATAAAGCAGTGAGTACTTACAGTATTTCCTGATT 181
Db      109 GlyMetProValTrp-----LeuIle 115
QY      182 GGGCTCTATACATTTCTAAGTCTTTTGGCTTTATGGGAATCTACTTATTTAAATGGCT 241
Db      116 ProSerTyrrMetIleLeuLeuPheAlaValLeuGlyAsnLeuValIleSerThr 135
QY      242 CTCATGAAAAGCGTAAATCAGAAGACTAGGTAACTTCTCATAGGCAATCTGCCCTTT 301
Db      136 LeuValGlnAsnArgMetArgThrIleThrAsnValPheLeuLeuAsnLeuAlaIle 155
QY      302 TCTGATATCTTGTGCTGCTGTTTGCCTCACCTTTTCACACTGACCTCTCTTGTGTGGAT 361
Db      156 SerAspMetLeuLeuGlyValLeuCysMetProValThrLeuValGlyThrLeuLeuArg 175
QY      362 CAGTGGATGTTGGCAAGTCATGTCATATATATGCTTTTCTTCATGTCAGTTCAGTT 421
Db      176 AsnPheIlePheGlyGluPheLeuCysLysLeuPheGlnPheSerGlnAlaAlaSerVal 195
QY      422 TTGGTTTCAACTTAAATTTAATATCAATTCGCAATGTTCAGGTATCATATGATAAACAAT 481
Db      196 AlaValSerSerTrpThrLeuValAlaIleSerCysGluArgTyrrAlaIleCysHis 215
QY      482 CCATATCTAATAAT-----TTAACAGCAACACCTGCTACTTCTTATGTCAGTACTGTC 535
Db      216 ProLeuArgSerArgSerTrpGlnThrIleSerHisAlaTyrrLysIleIleGlyPheIle 235
QY      536 TGGACACTAGGTTTGGCCATCTGTTCCCTTCCAGTGTTCACAGTCTTCTGGAACCTT 595
Db      236 TrpLeuGlyGlyLeuLeuCysMetThrProIleAlaValPheSerGlnLeuIlePro--- 254
QY      596 CAAGAAACATTTGGTTCAGCATTGTCAGCAGCAGC-----TATTATGTTGAG 646
Db      255 -----ThrSerArgProGlyTyrrCysLysCysArgGlu 265
QY      647 TCATGGCCATCTGATTATCATACAGATTCGCTTTACTATCTCTTTTATTGCTAGTACGAT 706
Db      266 PheTrpProAspGlnGlyTyrrGluLeuPheTyrrAsnIleLeuLeuAspPheLeuLeu 285
QY      707 ATTCTGCCCTTAGTTTGTCTTACTTACTAAGTCTCATACAAGTGTCTGCAGAGATATAAGCTGT 766
Db      286 ValLeuProLeuLeuValLeuCysValAlaTyrrIleLeuIleThrArgThrLeuTyrrVal 305
QY      767 GGATTGTCACAAACAAAGAAACAGAG---CTTGAAGAAATGAGATGATCACTTAACCTCTT 823
Db      306 GlyMetAlaLysAspSerGlyArgIleLeuGlnGlnSerLeuProValSerAlaThrThr 325
QY      824 CATCCATCCAAAGAGAGTGGGCTCAGGTGAAACTCTCTGGCAGCCATAAATGGAGTTAT 883
Db      326 AlaGlyGlySerAlaProAsnProGlyThr----- 335
QY      884 TCATTATCAAAAAACACAGAAAGAGATATAGCAAGAAGACAGCAGCATGTGTGTTA----- 937
Db      336 -----SerSerSerSerAsnCysIleLeuValLeu 345
QY      938 -----CCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGATAACTTCCAGAA 988
Db      346 ThrAlaThrAlaValTyrrAsnGlnAsnSerAsnAsnAsnGlyAsnSerGluGlySer 365
QY      989 AACTTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTCATACACGGGGTCCCC 1048
Db      366 AlaGlyGlyGlySerThrAsnMetAlaThrThrThrThrThrThrThrThrThrThr 385
QY      1049 ACTTGCTTTGAGATA-----AAACCTGAAGAAAT 1078

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|    |      |  |      |
|----|------|--|------|
| QY | 323  | TTTTGCTCACCTTTACACTGAGCTGTCTCTTGCTGGATCAGTGGATGTTTGTCGAAGTC    | 382  |
| DB | 93   | PheCysMetProPheAsnLeuIleProAsnLeuLeuLysAaspHelepHeGlySerAla    | 112  |
| QY | 383  | ATGTGCATATTATGCGCTTTCTTCAATGTGTCTCAGTTTGGTTTCAACTTTTAATTTTA    | 442  |
| DB | 113  | ValCysLysThrThrThyPheMetGlyThrSerValSerValSerThrPheAsnLeu      | 132  |
| QY | 443  | ATAATCATTCGCCATTGTCCAGGTATCATATGATAAAACATCCCATATCTAATAATTTA    | 499  |
| DB | 133  | ValAlaIleSerLeuGluArgTyGlyAlaIleCysArgProLeuGlnSerArgValTrp    | 152  |
| QY | 500  | ---ACAGCAAACCATGGCTACTTTCTGATAGTACTGTCTGGACACTAGAGTTTGGCATC    | 556  |
| DB | 153  | GlnThrLysSerHisAlaLeuLysValIleAlaAlaThrTrpCysLeuSerPheThrIle   | 172  |
| QY | 557  | TGTTCTCCCCCTCCAGNGTTTCACAGTCTGTGGAACCTTCAAGAAAACATTTGCTTCAGCA  | 616  |
| DB | 173  | MetThrProTyrrProIleTyrrSerAsnLeuValProPheThrLysAsnAsnGlnThr    | 192  |
| QY | 617  | TTGCTGAGCAGCAGGTATTTATGTGTGTGAGTCATGCCCATTCTGATTCATACAGAATGCC  | 676  |
| DB | 193  | AlaAsnMetCysArgPheLeuLeu-----ProSerAspAlaMetGlnGlnSer          | 208  |
| QY | 677  | TTTACTATCTTTATTGCTAGTTCAGTATATCTGCCCTTAGTTGCTCTTACTGTAAGT      | 736  |
| DB | 209  | TrpGlnThrPheLeuLeuLeuIleLeuPheLeuIleProGlyValValMetValValAla   | 228  |
| QY | 737  | CATACRAGTGTCTGCAGAAAGTATAAGCTGTGGATTGTCCAACAAGAAAAACAGACTTGAA  | 796  |
| DB | 229  | TyrGlyLeuIleSerLeuGluLeuTyrrGlnGlyIleLysPheAspAlaSerGin----    | 246  |
| QY | 797  | GAANAATGAGATGATCAACTTAACTCTTCATCCATCCAAAAAGAGTGGCGCTCAGGTGAAA  | 856  |
| DB | 247  | -----LysLysSerAlaLysGluLysArg                                  | 254  |
| QY | 857  | CTCTCT-----GGCAGCCATAAATGGAGTTATTCATTCATCAAAAAACACAGAAGA       | 907  |
| DB | 255  | LeuSerSerGlyGlyGlyGlyGlyGlySerSerSer-----Ser                   | 268  |
| QY | 908  | AGATATAGCAAGAAGACAGCATGTGTGTACCTGCTCCAGAAAAGACCTTCTCAAGAGAAC   | 967  |
| DB | 269  | ArgTyrrGluAspSerAspGlyCystyrrLeuGlnLysSerArgProProArgLysLeuGlu | 288  |
| QY | 968  | CACTCCAGAATCTTCCAGAAAACCTTTGGCTGTGTAAAGAGTCAGCTCTCTTTCATCCAGT  | 1027 |
| DB | 289  | -----LeuGlnGlnLeuSerThrSerSer                                  | 296  |
| QY | 1028 | AAGTTCATACCAGGGTCCCACCTTGCTTTTCAGATAAACCTGAAGAAAATTCAGATGTT    | 1087 |
| DB | 297  | -----SerGlyGlyArgIle   | 301  |
| QY | 1088 | CATGAATTGAGAGTAAACCGTTCTGTTCAGAAATAAAAAAGAGATCTCGAAGTGTTTTC    | 1147 |
| DB | 302  | AsnArgIleArgSerSerGlySerAlaAlaAsnLeuIleAlaLysLysArg---ValIle   | 320  |
| QY | 1148 | TACAGACTGACCATCTGATATTAGTATTGTCTGTAGTTGGATGCCACTACACCTTTTC     | 1207 |
| DB | 321  | ArgMetLeuIleValIleValIleValIlePheLeuCysTrpMetProIlePheSerAla   | 340  |
| QY | 1208 | CATGTGGTAACTGATTTTAATGCAACATCTTTATTTCAATAGGCCATTTTCAAG-----    | 1258 |
| DB | 341  | AsnAlaTrpArgAlaTyrr--AspThrValSerAlaGluLysHisLeuSerGlyThrPro   | 359  |
| QY | 1259 | TTGGTGTATGTCATTTGCTTCATTTCTGGCGATGATGCTCTGTCTTAAATCCCAATCTTA   | 1318 |
| DB | 360  | IleSerPheIleLeu-----LeuLeuSerTyrrThrSerSerCysValAsnProIleIle   | 377  |
| QY | 1319 | TATGGGTTTCTTAATAATGGGATTAAGAGCTGATTAGTGTCCCTTATACACTGT         | 1372 |
| DB | 378  | TyrCysPheMetAsnLysArgPheArgLeuGlyPheMetAlaThrPheProCys         | 395  |

S50150  
gastric CCK-A receptor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Apr-2000  
C:Accession: S50150  
R:Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.  
Biochim. Biophys. Acta 1219, 321-327, 1994  
A:Title: Cloning and expression of the rabbit gastric CCK-A receptor.  
A:Reference number: S50150; MUID:95002144; PMID:7918628  
A:Accession: S50150  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-427 <REU>  
C:Superfamily: neurokinin 1 receptor

Alignment Scores:  
Pred. No.: 2,11e-25 Length: 427  
Score: 375.00 Matches: 104  
Percent Similarity: 43.81% Conservative: 73  
Best Local Similarity: 25.74% Mismatches: 155  
Query Match: 15.12% Indels: 72  
DB: 2 Gaps: 9

US-09-771-956-4 (1-1406) x S50150 (1-427)

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|----|-----|--|-----|
| QY | 185 | CTCTATACATTGTAAGTCTCTTGGCTTTATGGGAATCTACTATTATTAATGGCTCTC    | 244 |
| Db | 47  | LeuTyrSerLeuIlePheLeuLeuSerValLeuGlyAsnThrLeuValIleThrValLeu | 66  |
| QY | 245 | ATGAAGAAAGCGTAATCAAGACATACGGTAACCTCTCATAGCAATCTGGCCCTTTCT    | 304 |
| Db | 67  | IleArgAsnLysArgMetArgThrValThrAsnIlePheLeuLeuSerLeuAlaIleSer | 86  |
| QY | 305 | GATATCTGGTGTGCTGTTTGTCTACCTTTTCACATGACGTCTGCTGCGATCAG        | 364 |
| Db | 87  | AspLeuMetLeuCysLeuPheCysMetProPheAsnLeuIleProAsnLeuLeuLysAsp | 106 |
| QY | 365 | TGGATGTTTGGCAAGTCATGTCATATATGCTTTCTTCAATGTGTGTCAGTTTG        | 424 |
| Db | 107 | PheIlePheGlySerAlaLeuCysLysThrThrThrLysMetGlyThrSerValSer    | 126 |
| QY | 425 | GTTTCAACTTTAATTAATCAATTCCTCCATGTCAGGTATCATATGATAAACAATCCC    | 484 |
| Db | 127 | ValSerThrLeuAsnLeuValAlaIleSerLeuGluArgTyrGlyAlaIleCysLysPro | 146 |
| QY | 485 | ATATCTAATAATTTA-----ACAGCAACCATGGCTACTTCTGTAGTACTGCTGG       | 538 |
| Db | 147 | LeuGlnSerArgValTrpGlnThrLysSerHisAlaLeuLysValIleAlaAlaThrTrp | 166 |
| QY | 539 | ACACTAGTTTGGCATCTGTTCTCCCTTCCAGTGTTCACAGTCTGTGGAACTTCAA      | 598 |
| Db | 167 | CysLeuSerPheAlaIleMetThrProTyrProIleTyrSerAsnLeuValProPheThr | 186 |
| QY | 599 | GAACATTTGTTGAGCATGCTGAGCAGCAGGTATTATTGTTGTTGAGTCAATGCCATCT   | 658 |
| Db | 187 | LysThrAsnAsnGlnThrAlaAsnMetCysArgPheLeuLeu-----ProSer        | 202 |
| QY | 659 | GATTTCATACAAATGGCTTTTACTATCTCTTTATTGCTAGTATATCTTGCCTTTA      | 718 |
| Db | 203 | AspValMetGlnGlnAlaTrpHisThrPheLeuLeuLeuIleLeuPheLeuIleProGly | 222 |
| QY | 719 | GTTTGTCTTACTGTAAGTATACAAAGTGTCTGCGAAGTATAGCTGTGGAATGTCACAC   | 778 |
| Db | 223 | IleValMetMetValAlaTrp-----                                   | 229 |
| QY | 779 | AAAGAAACACAGACTTGAAGAAATGACATGATCAACTTAACTTCTTCATCCATCAAAAAG | 838 |
| Db | 230 | -----GlyMetIleSerLeuGluLeuTyrGlnGly-----                     | 239 |
| QY | 839 | AGTGGGCTCAGGTGAACCTCTCTGGCAGCCATAATGGAGTTATTTCATTCATAAAA     | 898 |
| Db | 240 | -----IleLysPheAspAlaSerGlnLysLysSer-----AlaLys               | 251 |

|    |      |   |      |
|----|------|---|------|
| QY | 899  | CACAGAAGA-----AGATATAGCAAGACAGACATGTGTGTACTCT                 | 940  |
| Db | 252  | GlutArgLysAlaSerThrGlySerGlyArgPheGluAspAsnAspGlyCysTyrLeuGln | 271  |
| QY | 941  | GCTCCAGAAGACCTTCTCAAGAACCACTCCAGAATACCTCCAGAAAACCTTGGCTCT     | 1000 |
| Db | 272  | Arg---SerLysProThrArgGlnLeuGluLeuGlnLeuSerGlyGlyGlyGly        | 290  |
| QY | 1001 | GTAAGAAGTCAGCTCTCTTCTCCAGTAAGTTTCATACCAGGGGTCCCACTTGTCTTGAG   | 1060 |
| Db | 291  | ArgValSerArgIleHisSerSer-----                                 | 298  |
| QY | 1061 | ATAAACCTGAAGAAATTCAGATGTTTCATGAATTCAGAGTAAACGTTTGTTCACAGA     | 1120 |
| Db | 299  | -----SerSerAlaAlaLeuMetAlaLysLysArgValIleArg                  | 312  |
| QY | 1121 | ATAAAAAAGAGATCTCGAAGTGTTCCTACAGACTGACATATCATATTAGTATTGCT      | 1180 |
| Db | 313  | Met-----LeuMetValIleValLeuPhePhe                              | 322  |
| QY | 1181 | GTTAGTGGATCCCACTACACCTTTCCATGTGGTAAGTATTTTAATGACAAATCTTATT    | 1240 |
| Db | 323  | LeuCysTrpMetProIlePheSerAlaAsnAlaTrpArgAlaTyrAspThrValSerAla  | 342  |
| QY | 1241 | TCAATAGGCATTTCAAGTGTGTGCTGTTGCTATTCATTTGTTGGGCATGATGCTCTGT    | 1300 |
| Db | 343  | GluArgArgLeuSerGlyThrProIleSerPheIleLeuLeuLeuSerTyrThrSerSer  | 362  |
| QY | 1301 | TGCTTTAATCCAAATCTATATGGTTCCTTAATATGGGATTAAGCTGATTAGTGTCC      | 1360 |
| Db | 363  | CysValAsnProIleIleTyrCysPheMetAsnLysArgPheArgLeuGlyPheMetAla  | 382  |
| QY | 1361 | CTTATACACTGT  | 1372 |
| Db | 383  | ThrPheProCys  | 386  |

RESULT 14  
A42685  
cholecystokinin receptor type A - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A42685; J04225; PC2213  
R:Wank, S.A.; Harkins, R.; Jensen, R.T.; Shapira, H.; de Weerth, A.; Slatery, T.  
Proc. Natl. Acad. Sci. U.S.A. 89, 3125-3129, 1992  
A:Title: Purification, molecular cloning, and functional expression of the cholecystokinin  
A:Reference number: A42685; MUID:92212981; PMID:1313582  
A:Accession: A42685  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-444 <WAN>  
A:Experimental source: pancreas  
A:Note: sequences extracted from NCBI backbone (NCBI:93814, NCBI:93815)  
R:Takata, I.; Takiguchi, S.; Funakoshi, A.; Kono, A.  
Biochem. Biophys. Res. Commun. 213, 958-966, 1995  
A:Title: Gene structure of rat cholecystokinin type-A receptor.  
A:Reference number: J04225; MUID:95382845; PMID:7654260  
A:Accession: J04225  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-223 <TAK>  
A:Cross-references: DBJ:050608; NID:gl100752  
R:Mantamadiotis, T.; Baldwin, G.S.  
Biochem. Biophys. Res. Commun. 201, 1382-1389, 1994  
A:Title: The seventh transmembrane domain of Gastrin/CCK receptors contributes to non-pep  
A:Reference number: PC2213; MUID:94296413; PMID:8024583  
A:Accession: PC2213  
A:Status: preliminary  
A:Molecule type: protein  
C:Comment: This G-protein-coupled receptor is present in the gastrointestinal system, vas  
, smooth muscle contraction of the gallbladder and stomach. It is capable of activating i  
during the subsequent release of intracellular calcium.

Db 262 -----LysLysSerAlaLysGIuLysLys 269  
 QY 857 CTCTCT---GGCAGCCATAAATGAGGTATTCTATTCATCAAAAAACACAGAGAAGATAT 913  
 Db 270 ProSerThrGlySer-----SerThrArgTyr 278  
 QY 914 AGCAAGAAGACACGATCTGTGTTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCC 973  
 Db 279 GluAspSerAspGlyCysTyrLeuGlnLysSerArgProIbargLysLeuGIuLeuGln 298  
 QY 974 AGAATACTTCCAGAAACATTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTC 1033  
 Db 299 GlnLeuSerSerGlySerGlyGlySerArgLeuAsnArgIleArgSerSer----- 315  
 QY 1034 ATACCAAGGGTCCCACTGCTTTTGAGATAAAACCTCAAGAAAATTCAGATGTTTCATGAA 1093  
 Db 316 -----SerSerAlaAlaAsn 320  
 QY 1094 TTGAGAGTAAACGCTTCTGTTCACAGAATAAAAAAGAGATCTCGAAGTGTTCATACAGA 1153  
 Db 321 LeuIleAlaLysLysArgValIleArgMet----- 330  
 QY 1154 CTGACCACTGATATATGATTGCTGTAGTTGGATGGCCACTACACCTTTTCCCATGTG 1213  
 Db 331 LeuIleValIleValLeuPhePheLeuCysTrpMetProIlePheSerAlaAsnAla 350  
 QY 1214 GTAACGATTTTAATGACAATCTATTTCAAATAGGCATTTTCAAG-----TTGGTG 1264  
 Db 351 TrpArgAlaTyr---AspThrValSerAlaGIuLysHisLeuSerGlyThrProIleSer 369  
 QY 1265 TATTGCATTTGTCATTTGTTGGGCATGATGTCCTGTTGTCCTTAATCCAATTCATATATGGG 1324  
 Db 370 PheIleLeu-----LeuLeuSerTyrThrSerSerCysValAsnProIleIleTyrCys 387  
 QY 1325 TTCTCTTAATGCGATTAAGCTGATTTTAGTGTCCTTATACACTGT 1372  
 Db 388 PheMetAsnLysArgPheArgLeuGlyPheMetAlaThrPheProCys 403

RESULT 15  
 A41738  
 N:neuropeptide Y receptor - fruit fly (Drosophila melanogaster)  
 N:Alternate names: G protein-coupled receptor PR4  
 C:Species: Drosophila melanogaster  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
 C:Accession: A41738  
 R:Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.  
 J. Biol. Chem. 267, 9-12, 1992  
 A:Title: Cloning, functional expression, and developmental regulation of a neuropeptide Y receptor from Drosophila melanogaster  
 A:Reference number: A41738; MUID:92112730; PMID:1370455  
 A:Accession: A41738  
 A:Molecule type: mRNA  
 A:Residues: 1-449 <L1A>  
 A:Cross-references: UNIPROT:P25931; GB:M81490; NID:gl57996; PIDN:AAA26727.1; PID:1370455  
 C:Genetics:  
 A:Gene: FlyBase:NepYr  
 A:Cross-references: FlyBase:FBgn0004842  
 C:Superfamily: neurokinin 1 receptor  
 C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Alignment Scores:  
 Pred. No.: 1,1e-24 Length: 449  
 Score: 367.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 66  
 Best Local Similarity: 22.81% Mismatches: 123  
 Query Match: 14.80% Indels: 146  
 DB: 2 Gaps: 12

US-09-771-956-4 (1-1406) x A41738 (1-449)



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 21, 2004, 11:30:23 ; Search time 293.5 Seconds

(without alignments)  
5512.618 Million cell updates/sec

Title: US-09-771-956-4

Perfect score: 2480  
Sequence: 1 tttgtgtgtgcaaatgt.....attctcaactgtttaccaagg 1406

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p\_model -DEV=xlp  
-Q=/cgn\_1/USPRO\_pool\_P/US09771956/runat\_21102004\_103737\_9374/app\_query.fasta.1.1543  
-DB=Uniprot\_02 -QMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USPR=US09771956 @CGN 1 1 283 @runat\_21102004\_103737\_9374 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NSG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query | Length | DB | ID         | Description          |
|------------|--------|-------|--------|----|------------|----------------------|
| 1          | 2385   | 96.2  | 455    | 1  | NY5R HUMAN | Q15761 homo sapien   |
| 2          | 2330   | 94.0  | 445    | 2  | AAH42416   | AAH42416 homo sapi   |
| 3          | 2318   | 93.5  | 445    | 2  | Q9K73      | Q9K73 macaca mula    |
| 4          | 2241   | 90.4  | 446    | 2  | Q25F1      | Q25F1 cavia porce    |
| 5          | 2227   | 89.8  | 446    | 1  | NY5R CANFA | Q82729 canis fami    |
| 6          | 2084.5 | 84.1  | 456    | 1  | NY5R RAT   | Q83634 rattus norv   |
| 7          | 2070   | 83.5  | 466    | 1  | NY5R MOUSE | Q70342 mus musculu   |
| 8          | 2070   | 83.5  | 466    | 2  | BAC32426   | BAC32426 mus muscu   |
| 9          | 2028   | 81.8  | 446    | 1  | NY5R PIG   | Q97969 sus scrofa    |
| 10         | 1629.5 | 65.7  | 443    | 2  | Q8QF2      | Q8QF2 gallus gall    |
| 11         | 558    | 22.5  | 377    | 2  | O37733     | O37733 brachydanio   |
| 12         | 527    | 21.2  | 348    | 2  | Q8Y6A4     | Q8Y6A4 squalus aca   |
| 13         | 527    | 21.2  | 348    | 2  | AAO62565   | AAO62565 squalus aca |
| 14         | 522.5  | 21.1  | 373    | 2  | Q8Y6A5     | Q8Y6A5 squalus aca   |
| 15         | 522.5  | 21.1  | 373    | 2  | AAO62564   | AAO62564 squalus a   |
| 16         | 502.5  | 20.3  | 377    | 2  | Q8QGM3     | Q8QGM3 gallus gall   |

|    |       |      |     |   |            |                    |
|----|-------|------|-----|---|------------|--------------------|
| 17 | 497   | 20.0 | 371 | 1 | NY6R RABIT | P78217 oryctolagus |
| 18 | 487.5 | 19.7 | 382 | 1 | NY1R CANFA | O02813 canis fami  |
| 19 | 487.5 | 19.7 | 383 | 1 | NY1R PIG   | O02835 sus scrofa  |
| 20 | 484.5 | 19.5 | 385 | 2 | Q8QFM1     | Q8QFM1 gallus gall |
| 21 | 481.5 | 19.4 | 366 | 1 | NY1R XENLA | P34992 xenopus lae |
| 22 | 481.5 | 19.4 | 383 | 2 | Q9K75      | Q9K75 macaca mula  |
| 23 | 481.5 | 19.4 | 384 | 1 | NY1R HUMAN | P25929 homo sapien |
| 24 | 481.5 | 19.4 | 384 | 2 | AA55647    | AA55647 homo sapi  |
| 25 | 481.5 | 19.4 | 384 | 2 | AAH71720   | AAH71720 homo sapi |
| 26 | 481   | 19.4 | 383 | 1 | NY1R CAVPO | Q04573 mus musculu |
| 27 | 480   | 19.4 | 382 | 1 | NY1R MOUSE | P21555 rattus norv |
| 28 | 480   | 19.4 | 382 | 2 | AAH51420   | AAH51420 mus muscu |
| 29 | 480   | 19.4 | 382 | 2 | AAH51420   | O61212 mus musculu |
| 30 | 476   | 19.2 | 371 | 1 | NY6R MOUSE | BAC26875 mus muscu |
| 31 | 476   | 19.2 | 371 | 2 | BAC26875   | BAC26875 mus muscu |
| 32 | 473.5 | 19.1 | 385 | 1 | NY2R CHICK | Q90dn6 gallus gall |
| 33 | 471.5 | 19.0 | 374 | 2 | Q9YHX1     | Q9YHX1 gadus morhu |
| 34 | 466   | 18.8 | 375 | 2 | O97505     | O97505 sus scrofa  |
| 35 | 466   | 18.8 | 375 | 2 | Q6YHV0     | Q6YHV0 macaca mula |
| 36 | 466   | 18.8 | 375 | 2 | AAH28939   | AAH28939 macaca mu |
| 37 | 464.5 | 18.7 | 375 | 1 | NY4R HUMAN | P50391 homo sapien |
| 38 | 464.5 | 18.7 | 375 | 2 | Q6FH06     | Q6FH06 homo sapien |
| 39 | 464   | 18.7 | 375 | 1 | NY4R RAT   | Q63447 rattus norv |
| 40 | 464   | 18.7 | 375 | 2 | O57463     | O57463 brachydanio |
| 41 | 459   | 18.5 | 371 | 2 | Q6Y6A6     | Q6Y6A6 squalus aca |
| 42 | 459   | 18.5 | 371 | 2 | AAO62563   | AAO62563 squalus a |
| 43 | 458.5 | 18.5 | 381 | 2 | Q8BWL1     | Q8BWL1 mus musculu |
| 44 | 458.5 | 18.5 | 385 | 1 | NY2R MOUSE | P97295 mus musculu |
| 45 | 458   | 18.5 | 375 | 1 | NY4R MOUSE | Q61041 mus musculu |

#### ALIGNMENTS

##### RESULT 1

| NY5R_HUMAN   | STANDARD; | PRT; | 455 AA. |
|--|-----------|------|---------|
| ID Q15761; Q92916;   |           |      |         |
| DT 01-NOV-1997 (Rel. 35, Created)  |           |      |         |
| DT 01-NOV-1997 (Rel. 35, Last sequence update)   |           |      |         |
| DT 05-JUL-2004 (Rel. 44, Last annotation update)   |           |      |         |
| DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor) (NPY5).   |           |      |         |
| DE Names=NPY5R; Synonyms=NPYR5;  |           |      |         |
| OS Homo sapiens (Human).   |           |      |         |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |           |      |         |
| OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.   |           |      |         |
| OX NCBI_TaxID=9606;  |           |      |         |
| [1]  |           |      |         |
| RN SEQUENCE FROM N.A.  |           |      |         |
| RP TISSUE=Hippocampus;   |           |      |         |
| RC MEDLINE=96317589; PubMed=8700207;   |           |      |         |
| RA Gerald C., Walker M.W., Criscione L., Gustafson E.L.,   |           |      |         |
| RA Batzl-Hartmann C., Smith K.E., Vaysses P., Durkin M.M., Laz T.M.,   |           |      |         |
| RA Lineneyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G.,  |           |      |         |
| RA Taber R.I., Branchek T.A., Weinschank R.L.;   |           |      |         |
| RT 'A receptor subtype involved in neuroptide-Y-induced food intake.';   |           |      |         |
| RL Nature 382:168-171(1996).   |           |      |         |
| [2]  |           |      |         |
| RN SEQUENCE OF 11-455 FROM N.A.  |           |      |         |
| RP MEDLINE=96421636; PubMed=8824284;   |           |      |         |
| RA Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B.,  |           |      |         |
| RA Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L.,   |           |      |         |
| RA Sadowski Y., Schaefer J., Velazquez N., McCaleb M.L.;   |           |      |         |
| RT 'Identification of a novel hypothalamic neuroptide Y receptor associated with feeding behavior.';                                   |           |      |         |
| RL J. Biol. Chem. 271:26315-26319(1996).   |           |      |         |
| [3]  |           |      |         |
| RN SEQUENCE OF 11-455 FROM N.A.  |           |      |         |
| RP MEDLINE=97312686; PubMed=9169127;   |           |      |         |
| RA Herzog H., Darby K., Ball H., Hori Y., Beck-Sickinger A., Shine J.;   |           |      |         |
| RT 'Overlapping gene structure of the human neuroptide Y receptor subtypes Y1 and Y5 suggests coordinate transcriptional regulation.'; |           |      |         |
| RL Genomics 41:315-319(1997).  |           |      |         |

[4]  
 RN SEQUENCE OF 11-455 FROM N.A.  
 RA Kozak S.A., Aronstam R.S., Sharma S.V.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RL submitted (JUN-2003) to the EMBL/GenBank/DBJ databases."  
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity  
 CC of this receptor is mediated by G proteins that inhibit adenylylate  
 CC cyclase activity. Seems to be associated with food intake. Could  
 CC be involved in feeding disorders.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Brain; hypothalamus.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC Highest to tachykinins receptors.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U56079; AAC50623.1; -;  
 DR EMBL; U66275; AAC50741.1; -;  
 DR EMBL; U94320; AAC51295.1; -;  
 DR EMBL; AY322538; AAP84351.1; -;  
 DR Genbank; HGNC:7958; NPY5R;  
 DR MIM; 602001; -;  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO; GO:0004983; F: neuropeptide Y receptor activity; TAS.  
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . . ; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR000393; NPV5\_receptor.  
 DR InterPro; IPR000611; NPY\_receptor.  
 DR Pfam; PF00001; 7tm1; 1;  
 DR PRINTS; PR00237; GPCR\_HODOPSIN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; FALSE\_NEG.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F2\_1;  
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
 KW Phosphorylation; Transmembrane.  
 FT DOMAIN 1 50 Extracellular (Potential).  
 FT TRANSMEM 51 72 1 (Potential).  
 FT DOMAIN 73 84 Cytoplasmic (Potential).  
 FT TRANSMEM 85 105 2 (Potential).  
 FT DOMAIN 106 125 Extracellular (Potential).  
 FT TRANSMEM 126 147 3 (Potential).  
 FT DOMAIN 148 167 Cytoplasmic (Potential).  
 FT TRANSMEM 168 188 4 (Potential).  
 FT DOMAIN 189 220 Extracellular (Potential).  
 FT TRANSMEM 221 242 5 (Potential).  
 FT DOMAIN 243 378 Cytoplasmic (Potential).  
 FT TRANSMEM 379 401 6 (Potential).  
 FT DOMAIN 402 414 Extracellular (Potential).  
 FT TRANSMEM 415 438 7 (Potential).  
 FT DOMAIN 439 455 Cytoplasmic (Potential).  
 FT CARBOHYD 20 20 N-linked (GlcNAc. . . ) (Potential).  
 FT CARBOHYD 27 27 N-linked (GlcNAc. . . ) (Potential).  
 FT DISULFID 124 208 By similarity.  
 FT LIPID 452 452 S-palmitoyl cysteine (Potential).  
 SQ SEQUENCE 455 AA; 51990 MW; 95f2f47e5f8ff7 CRC64;  
 Alignment Scores:  
 Pred. No.: 2,696-188 Length: 455  
 Score: 2385.00 Matches: 455  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 96.17% Indels: 0  
 DB: 1 Gaps: 0  
 US-09-771-956-4 (1-1406) x NY5R\_HUMAN (1-455)  
 17 ATGCTCTTTTATCCAGCAGGACTATAATATGATTAGATTAGAGTCGACGAGTATTATAAC 76

Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20  
 QY 77 AAGACACTTGGCCACAGAGAAATAACTGCTGCACCTCGGAATTCCTGATTTCCAGCTCGG 136  
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40  
 QY 137 GATGACTATAAAGCAGGTGTAGATGACTTACAGTATTTTCTGATTTGGGCTCTATACATTT 196  
 Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60  
 QY 197 GTAAGTCCTCTTGGCTTTATGTTGGGAATCTACTATTATTAATGGCTCTCATCAAAAAGCGT 256  
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80  
 QY 257 AATCAGAGACTACGGTAAACTTCCTCATAGCAATCTGGCCTTTCTGATATCTTGTT 316  
 Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100  
 QY 317 GTGCTGTTTGTCTACCTTTACACTGAGCTGTCTTCTGGATCAGTGGATGTTGCG 376  
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120  
 QY 377 AAAGTCATGTGTCATATTATGCTTTCTTCAATGTGTGTCTGAGTTTGGTTTCAACTTTA 436  
 Db 121 LysValMetCysHisIleValMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140  
 QY 437 ATTTAAATATCAATTGCCATTGTCCAGTATCATATGATATAAACATCCCATCATTAATAT 496  
 Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160  
 QY 497 TTAACAGCAAAACATGGCTTACTTTCTGATAGTACTGTCTGGACACTAGGTTTGGCCATC 556  
 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180  
 QY 557 TGTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTTCAGCA 616  
 Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200  
 QY 617 TTGCTGACGACGAGGTATTATGCTGTGAGTCATGCGCATCGCCATCTGATTATACAGAAATGCC 676  
 Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220  
 QY 677 TTTACTATCTCTTTATGCTAGTTCAGTATATCTGCCCTTAGTTTGTCTTACTGTAAAGT 736  
 Db 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240  
 QY 737 CATACAGTGTCTGCAGAGATATAAGCTGTGGATTGTCCACAAAGAAACAGACTTCAA 796  
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsArgLeuGlu 260  
 QY 797 GAAATGAGATGATCAACTTAACTCTTCATCCATCCAAAAAGAGTGGGCCTCAGGTGAAA 856  
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280  
 QY 857 CTCTCTGGCAGCCATAAATGGAGTATTATTCATTCATCAAAAACAGACAGAGATATAGC 916  
 Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300  
 QY 917 AAGAAGACAGCATGTGTGTACTCTCCAGAAAGACCTTCTCAAGAGAAACACCTCCAGA 976  
 Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320  
 QY 977 ATACTTCCAGAAAACTTTGGCTCTCTAAGACTCAGCTCTCTTCTCATCAGTAAGTTCTATA 1036  
 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340  
 QY 1037 CCAGGGGTCCTCCACTTGTCTTGAGATAAAACCTCGAAGAAAATTCAGATGTTTCATGAATTTG 1096  
 Db 341 ProGlyValProThrCysPheGluLeuLysProGluGluAsnSerAspValHisGluLeu 360  
 QY 1097 AGAGTAAAAAGCTTCTGTTTACAGATAAAAGAGATCTCGAAGTGTCTTCTACAGACTG 1156



Db 361 ArgVallysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380  
 QY 1157 ACCATACTGATATTAGTATTGCTGGTTAGTTGGATGCCACTACACCTTTTCCATGTGTA 1216  
 Db 381 ThrIleLeuLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400  
 QY 1217 ACTGATTTTAATGCAATCTTATTTCAAATAGGCAATTCAGTTGGTGATTCGATTTGT 1276  
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420  
 QY 1277 CATTTGTTGGCAGTATGCTGCTGTTGCTTAATCCAAATTCATATGCTGTTCTTAATAAT 1336  
 Db 421 HisLeuLeuGlyMetMetSerCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
 QY 1337 GCGATTAAAGCTGATTAGTGTCCCTTATACACTGCTGCTTCATATG 1381  
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455  
 RESULT 2  
 AAH42416 PRELIMINARY; PRT; 445 AA.  
 ID AAH42416;  
 AC AAH42416;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Neuropeptide Y receptor Y5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshyuki S., Carncini P., Frange C.,  
 RA Raba S.S., Lequellano N.J., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the ENBL/GenBank/DBJ databases.  
 DR EMBL; BC042416; AAH42416.1; -;  
 KW Neuropeptide; Receptor.  
 SQ SEQUENCE 445 AA; 50726 MW; A2B0F3169DBA66BE CRC64;

## Alignment Scores:

Pred No.: 9,36e-184 Length: 445  
 Score: 2330.00 Matches: 445  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.95% Indels: 0  
 DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x AAH42416 (1-445)

QY 47 ATGAGTTTAGAGTCGACGAGTATTATACAAAGACACTTCCACAGAGAAATAACTGCT 106  
 Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20  
 QY 107 GCCACTCGGAATTCGATTTCCAGTCTGGGAGTACTATAAAGCAGCTGACGACTTA 166  
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40  
 QY 167 CAGTATTTTCTGATTTGGGCTCTATACATTGTAAAGTCTTCTTGGCTTTATGGGGAATCTTA 226  
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 QY 227 CTTATTTTAAATGGCTCTCATGAAAAAGCTAATCAGAGACTACGGTAAACTTCCTCAT 286  
 Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuIle 80  
 QY 287 GGCATCTCGCCCTTTCTCATATCTTGGTGTGGTCTTGTCTCACCTTTCACACTGAGC 346  
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValLeuPheCysSerProPheThrLeuThr 100  
 QY 347 TCTGCTTCTGTCGATCAGTGGATGTTTGGCAAGTCATGTGCCATATTATGCTTTTCTT 406  
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120  
 QY 407 CAATGTGCTCAGTTTGGTTTCAACTTTTAAATTAATCAATTGCCATTGTCAGGTAT 466  
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140  
 QY 467 CATATGATAAAACATCCCATATCTAATAATTTAAACAGCAAAACCATGGCTACTTTCTGATA 526  
 Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160  
 QY 527 GCTACTGTCTGGACACTAGTGTTCGCCATCTGTTCCCTTCCAGTGTTCACAGTCTT 586  
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
 QY 587 GTGGAACTTCAAGAAACATTTGCTTGCAGATTGCTGAGCAGCAGGTATTATTGTGTGAG 646  
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200  
 QY 647 TMATGCCATCTGATTCATACAGAAATGGCTTACTATCTCTTATCTTATGCTAGTTCAGTAT 706  
 Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220  
 QY 707 ATTCTGCCCTTAGTTGCTTACTGTAACTCATACAAGTGTCTGCAGAGAGTATAAGCTGT 766  
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
 QY 767 GGATTTCTCCAAACAAAGAAACACAGACTTGAAGAAAATGAGATGATCAACTTAATCTTCTAT 826  
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260  
 QY 827 CCATCCAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCCATAAATGGAGTATTATCA 886  
 Db 261 ProSerLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280  
 QY 887 TTTATCAAAAAACACAGAAAGAGATATAGCAAGAGACAGCATGTGTGTACTGCTCA 946  
 Db 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
 QY 947 GAAAGACCTTCTCAGAGAAACCACTCCAGAAATCTTCGAGAAACTTTGGCTCTGTAAAGA 1006  
 Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320  
 QY 1007 AGTCAGCTCTCTTTCATCCAGTAAGTTTCACACAGGGGTCCCACTTGTCTTTGAGATAAAA 1066  
 Db 321 SerGlnLeuSerSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340  
 QY 1067 CTTGAAGAAAATTCAGATCTTCATGAATTTGAGAGTAAACCGTTCTCTTTTCAAGAAATAAAA 1126  
 Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360  
 QY 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATATCTGATATTATTTCTGCTGTAGT 1186

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Db      ||||| 361 LysArgSerArgSerValPheTyrArgLeuThrLeuLeuLeuValPheAlaValSer 380
QY      ||||| 1187 TGGATGCCACTACACCTTTCCATGCTGGTAAGTATTAATGACAATCTTATTTCAAAT 1246
Db      ||||| 381 TrpMetProLeuHisLeuPheHisValThrAspPheAsnAspLeuLeuSerAsn 400
QY      ||||| 1247 AGGCAATTCAGTGGTGTATTCGATTGTGATTTGGCAGATGCTGTGCTT 1306
Db      ||||| 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 420
QY      ||||| 1307 AATCCAAATCTATATGGTTTCTTAATAATGGGATTAAGCTGATTAGTGTCCCTTATA 1366
Db      ||||| 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuLeu 440
QY      ||||| 1367 CACTGTCTTCATATG 1381
Db      ||||| 441 HisCysLeuHisMet 445

RESULT 3
Q9GK73 PRELIMINARY; PRT; 445 AA.
AC      Q9GK73;
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Neurotrophin Y receptor Y5.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecoidea; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21184974; PubMed=11287088;
RA      Gehlert D.R., Yang P., George C., Wang Y., Schober D.,
RA      Gackenhelmer S., Johnson D., Beavers L.S., Galski R.A., Baez M.;
RT      "Cloning and characterization of Rhesus monkey neurotrophin Y receptor
RT      subtypes (1).";
RL      Peptides 22:343-350 (2001).
DR      EMBL; AF303031; AAG40773.1;
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0004983; F:neurotrophin Y receptor activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR      GO; GO:0007218; P:neurotrophin signaling pathway; IEA.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      InterPro; IPR000393; NPY5_Receptor.
DR      InterPro; IPR000611; NPY_Receptor.
DR      Pfam; PF00001; 7tm_1;
DR      PRINTS; PR00237; GPCR_Rhodopsn.
DR      PRINTS; PR01016; NRPEPTIDEYR.
DR      PRINTS; PR01012; NRPEPTIDEYR.
DR      PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW      Neurotrophin Y Receptor
SQ      SEQUENCE 445 AA; 50812 MW; ASDACD259675BC93 CRC64;

Alignment Scores:
Pred. No.: 9.17e-183 Length: 445
Score: 2318.00 Matches: 442
Percent Similarity: 99.78% Conservative: 2
Best Local Similarity: 99.33% Mismatches: 1
Query Match: 93.47% Indels: 0
DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x Q9GK73 (1-445)

QY      ||||| 47 ATGATTTAGAGCTCGACGAGTATTATAAAGACACTTGGCAGAGAGATAATACGTCT 106
Db      ||||| 1 MetAspLeuGluLeuAspGlyTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
QY      ||||| 107 GCCACTCGGAATTCGATTTCCAGTCTGGGATGACTATATAAGCAGTGTAGATCTTA 166

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Db      ||||| 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
QY      ||||| 167 CAGTATTTCTGATGGGCTCTATACATTTGTAGTCTCTTGGCTTTATGGGNAATCTA 226
Db      ||||| 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
QY      ||||| 227 CTTATTTAATGGCTCTCATGAAAGCGTAAATCAGAGACTACAGTAAACTTCTCTATA 286
Db      ||||| 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeuLeu 80
QY      ||||| 287 GGCATCTGGCCCTTTCTCATATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 346
Db      ||||| 81 GlyAsnLeuAlaPheSerAspIleLeuValLeuPheCysSerProPheThrLeuThr 100
QY      ||||| 347 TCTGTCTGCTGGATCAGTGGATGTTTGGCAAGTCATGTGCCATATATATATATATATATATAT 406
Db      ||||| 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisLeuMetProPheLeu 120
QY      ||||| 407 CAATGTGTGTGAGTTTGTGTTTCACTTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 466
Db      ||||| 121 GlnCysValSerValLeuValSerThrLeuLeuLeuIleSerIleAlaIleValArgTyr 140
QY      ||||| 467 CATATGATAAATCATCCCATATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 526
Db      ||||| 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuLeu 160
QY      ||||| 527 GCTACTGTCTGGACACTAGTGTGTGCTTCCCATCTGTTCTCCCTTCCAGTGTTCACAGTCTT 586
Db      ||||| 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
QY      ||||| 587 GTGGAATCTCAAGAAACATTTGGTTCACGATTTGCTGACAGCAGGATTTATGTTGAG 646
Db      ||||| 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
QY      ||||| 647 TCATGGCATCTGATTATACAGAAATTCCTTACTATCTCTTTTATCTAGTTCAGTAT 706
Db      ||||| 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuLeuValGlnTyr 220
QY      ||||| 707 ATTCTGCCCTTAGTTGTCTTACTTAAGTTCATACAGTGTCTGACAGGATTTAAGCTGT 766
Db      ||||| 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
QY      ||||| 767 CAGTTGTCCAAAGAAACAGACTTCAAGAAATAGATGATCACTTAACCTTCTTCTTCTTCTTCT 826
Db      ||||| 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
QY      ||||| 827 CCATCCAAAAGAGTGGGCTCAGGTGAAACTCTCTGCGAGCCATATAATGAGGTATTCA 886
Db      ||||| 261 ProSerArgLysIleGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280
QY      ||||| 887 TTCATCAAAAACACAGAGAAGATATAGCAAGACAGCAGATGTGTGTACCTGCTTCA 946
Db      ||||| 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
QY      ||||| 947 GAAAGACCTTCTCAAGAGAACCACTCCAGATACTTCCAGAAAACCTTGGCTCTGTAGA 1006
Db      ||||| 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
QY      ||||| 1007 AGTCAGCTCTCTTTCATCCAGTAAGTTCATACAGGGGTCCCGCTGTTGTTGAGTAAA 1066
Db      ||||| 321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340
QY      ||||| 1067 CCGTGAAGAAAATTCAGATGTTTCATCAATTGAGAGTAAACGTTCTGTGTACAGAAATAAAA 1126
Db      ||||| 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360
QY      ||||| 1127 AAGAGATCTCGAAGTGTCTTCTACAGATGACCATCTGATATAGTATTTGCTGTAGT 1186
Db      ||||| 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuLeuValPheAlaValSer 380
QY      ||||| 1187 TCGATGCCACTACACTTTTCCATGTGTAAGTATTTAATGACAACTTTATTTTCAAT 1246
Db      ||||| 381 TrpMetProLeuHisLeuPheHisValThrAspPheAsnAspAsnLeuLeuSerAsn 400

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QY 1247 AGGATTCAGTTGGTGTATGATTTGATTTGATTTGGCGATGATGCTGTTGCTT 1306  
 DB 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLeu 420  
 QY 1307 AATCCAAATTCATATGCTTTCTTAATAATGGGATTAAAGTGATTTAGTGCTCCCTTATA 1366  
 DB 421 AsnProLeuLeuGlyPheLeuAsnAsnGlyIleLysAlaAspLeuMetSerLeuLeu 440  
 QY 1367 CACTGCTTCATATG 1381  
 DB 441 HisCysLeuHisMet 445

RESULT 4  
 Q925F1 PRELIMINARY; PRT; 446 AA.  
 AC Q925F1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE NPV receptor 5.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21184976; PubMed=11287090;  
 RA Lundell I., Eriksson H., Marklund U., Larhammar D.;  
 RT "Cloning and characterization of the guinea pig neuropeptide Y  
 receptor Y5.";  
 RL Peptides 22:357-363(2001).  
 DR EMBL; AF363240; AAK52800.1; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR000393; NPV5\_receptor.  
 DR InterPro; IPR000611; NPV\_receptor.  
 DR Pfam; PF00001; 7cm1; 1.  
 DR PRINTS; PRO0237; GPCRHOPOPSN.  
 DR PRINTS; PRO1016; NRPEPTIDEY5R.  
 DR PRINTS; PRO1012; NRPEPTIDEYR.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 446 AA; 50936 MW; 2C3984B0A90AA693 CRC64;

Alignment Scores:  
 Pred. No.: 2,1e-176 Length: 446  
 Score: 2241.00 Matches: 425  
 Percent Similarity: 97.75% Conservative: 10  
 Best Local Similarity: 95.51% Mismatches: 10  
 Query Match: 90.36% Indels: 0  
 DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x Q925F1 (1-446)

QY 47 ATGGATTTCAGCTCGAGAGTATTATAAAGACCTTGCCACAGAGATAATACCTGCT 106  
 DB 1 MetAspLeuGluLeuLysGluTyrAsnLysThrLeuAlaThrGluAsnAsnThrThr 20  
 QY 107 GCCACTCGGAATTCGATTTCCAGCTCGGATGACATATAAAGCATGTAGATGACTTA 166  
 DB 21 ThrThrArgAsnSerAspPheProValTyrAspAspTyrArgSerSerValAspLeu 40  
 QY 167 CAGATTTTCGATGGCTCATACATTTGTAGTCTCTTGGCTTTATGGGAATCTA 226  
 DB 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 QY 227 CTTATTTTAAATGGCTCTCATGAAAAGCGTAATCAGAAGACTACGGTAAATCTCCTCAT 286

DB 61 LeuIleLeuMetAlaLeuIleLysLysArgAsnGlnLysThrThrValAsnPheLeuLeu 80  
 QY 287 GCAATCTGGCTTTTCTGATATCTTGTTGCTGTTTGTCTCACCTTTTCACACTGAGC 346  
 DB 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100  
 QY 347 TCTGCTCTGCTGATCAGTGGATTTGGCAAGTCATGTCGCATATATATGCTTTCTT 406  
 DB 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120  
 QY 407 CAATGTGTCTCAGTTTGGTTTCAACTTTAAATTTAATATCAATTCAGGTAT 466  
 DB 121 GlnCysValSerValLeuValSerThrLeuIleLeuSerIleAlaIleValArgTyr 140  
 QY 467 CATATGATTAACATCCCATATCTAATAATTAACAGCAACCATGGCTACTTCTGATA 526  
 DB 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuLeu 160  
 QY 527 GCTACTGTCTGGACACTAGTGTTCCTCTCTCCCTTCCAGTGTTCACAGTCTT 586  
 DB 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
 QY 587 GTGGAACTTCAAGAAACATTTGGTTTCAGATTTGCTGAGCAGCAGGTATTTATGTTGAG 646  
 DB 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200  
 QY 647 TCATGCCATCTGATTCATACAGAAATGCTTTACTATCTCTTTTATTGCTAGTTCAGTAT 706  
 DB 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220  
 QY 707 ATTCTGCCCTTAGTTGCTTACTACTAGTCATACAAAGTGTCTGCAGAGTATAGCTGT 766  
 DB 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
 QY 767 GGATTTGCTCAACAAAGAAACAGATTCGAGAAATAGATCATCACTTACTTCTTCAAT 826  
 DB 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260  
 QY 827 CCATCCAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCAATAAATGGAGTTATTC 886  
 DB 261 ProSerLysLysSerGlyAsnGlnValLysLeuSerLysThrHisLysTrpSerTyrSer 280  
 QY 887 TTCATCAAAAAACACAGAGAGATATAGCAGAGACAGCATGTGTGTTCTCTCTCCA 946  
 DB 281 PheIleArgLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
 QY 947 GAAAGACCTTCTCAAGAGAACCACTCCAGATCTCCAGAAAACCTTTGGCTCTGTAAGA 1006  
 DB 301 AlaArgProSerLeuGluAsnGlnSerArgThrLeuProGluAsnPheGlySerValArg 320  
 QY 1007 AGTCAGCTCTCTCATCCAGTAAGTTTCATACCAGGGGTCCCACTTGTCTTGAGATAAAA 1066  
 DB 321 SerGlnIleSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340  
 QY 1067 CCTGAAGAAATTCAGATGTTTCATGAATTTGAGAGTAAACGTTCTGTACAGAATAAAA 1126  
 DB 341 ProGluAspAsnSerAspAlaHisGluMetArgValLysArgSerIleThrArgIleLys 360  
 QY 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTAGATATTAGTATTTCTGTACT 1186  
 DB 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuLeuValPheAlaValSer 380  
 QY 1187 TGGATGCCACTACACCTTTTCCATGTTGTAAGTATTAATGACATCTTATTCAAT 1246  
 DB 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400  
 QY 1247 AGGCATTTTCAAGTGTGTATTGCTATTTGCTATTGTTGGGATGATGCTTGTGTCTT 1306  
 DB 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLeu 420  
 QY 1307 AATCCAAATTCATATGCTTTCTTAATAATGGGATTAAAGCTATTAAGTGTAGTCTTATA 1366  
 DB 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuMetSerLeuLeu 440

QY 1367 CACTGTCTTCATATG 1381  
 DB 441 HisCysLeuHisLeu 445

RESULT 5  
 NY5R CANFA STANDARD; PRT; 446 AA.  
 AC 062729;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5  
 DE receptor) (NPY5)  
 GN Name=NPY5R; Synonyms=NPY5;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_taxid=9615;  
 RN [1]  
 RZ SEQUENCE FROM N.A.  
 RX MEDLINE=99017379; PubMed=9802393;  
 RA Bowsky B., Walker M.W., Bard J., Weinshank R.L., Laz T.M.,  
 RA Voyse P., Branchek T.A., Gerald C.;  
 RT "Molecular biology and pharmacology of multiple NPY Y5 receptor  
 species homologs";  
 RL Regul. Pept. 75:45-53(1998).  
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity  
 CC of this receptor is mediated by G proteins that inhibit adenylate  
 CC cyclase activity. Seems to be associated with food intake. Could  
 CC be involved in feeding disorders (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC Highest to tachykins receptors.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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 DR EMBL; AF049328; AAC17838.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR000393; NPY5\_receptor.  
 DR InterPro; IPR000611; NPY\_receptor.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHOODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; FALSE\_NEG.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR G-protein coupled receptor; Gycoprotein; Lipoprotein; Palmitate;  
 KW Phosphorylation; Transmembrane.  
 FT DOMAIN 1 40 Extracellular (Potential).  
 FT TRANSMEM 41 62 1 (Potential).  
 FT DOMAIN 63 74 Cytoplasmic (Potential).  
 FT TRANSMEM 75 95 2 (Potential).  
 FT DOMAIN 96 115 Extracellular (Potential).  
 FT TRANSMEM 116 137 3 (Potential).  
 FT DOMAIN 138 157 Cytoplasmic (Potential).  
 FT TRANSMEM 158 178 4 (Potential).  
 FT DOMAIN 179 210 Extracellular (Potential).  
 FT TRANSMEM 211 232 5 (Potential).  
 FT DOMAIN 233 368 Cytoplasmic (Potential).  
 FT TRANSMEM 369 391 6 (Potential).  
 FT DOMAIN 392 404 Extracellular (Potential).  
 FT TRANSMEM 405 428 7 (Potential).  
 FT DOMAIN 429 446 Cytoplasmic (Potential).  
 FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 17 17 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 114 198 By similarity.  
 FT LIPID 442 442 S-palmitoyl cysteine (Potential).  
 SQ SEQUENCE 446 AA; 51012 MW; 5CAC8D2FCF5D254A CRC64;

Alignment Scores: 3.01e-175 Length: 446  
 Pred. No.: 2227.00 Matches: 422  
 Score: 97.30% Conservative: 11  
 Percent Similarity: 94.83% Mismatches: 12  
 Best Local Similarity: 89.80% Indels: 0  
 Query Match: 1 Gaps: 0  
 DB: 1

US-09-771-956-4 (1-1406) x NY5R\_CANFA (1-446)

QY 47 ATGGATTAGAGCTGACGAGTATTATACAGACACTTGCACAGAGAAATAACTGCT 106  
 DB 1 MetAspLeuGluLeuGlnAspPheYrAsnLysThrLeuAlaThrGluAsnThrAla 20  
 QY 107 GCACCTCGGAATTCGATTCCCACTCTGGGAGTACTATAAAGCAGGTGTAGACTTA 166  
 DB 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40  
 QY 167 CAGTATTTCTGATTGGGCTCTATACATTCTTGAAGTCTTCTTGGCTTTATGGGAATCTA 226  
 DB 41 GlnTyrPheLeuLeuLeuLeuLeuTyrThrPheValSerLeuLeuGlyPheMetCysAsnLeu 60  
 QY 227 CTTATTTTAATGGCTCTCATGAAAGGCTAATCAGAGACTTACGGTAAACTTCTCATA 286  
 DB 61 LeuLeuLeuMetAlaLeuMetArgLysArgAsnGlnLysThrMetValAsnPheLeuLeu 80  
 QY 287 GGCATCTGGCCTTTTCTGATATCTTGGTTGCTGCTTGTGCTCACCCTTACACTGAGG 346  
 DB 81 GlyAsnLeuAlaPheSerAspLeuValValLeuPheCysSerProPheThrLeuThr 100  
 QY 347 TCTGCTCTGCTGATCAGTGGATGTTTGGCAAGTCATGTGCCATATTATGCTTTTCTT 406  
 DB 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisLeuMetProPheLeu 120  
 QY 407 CAATGTGTCTAGTTTGGTTTCAACTTAATTTAATCAATTCGCAATTCAGGTAT 466  
 DB 121 GlnCysValSerValLeuValSerThrLeuLeuLeuLeuSerLeuAlaLeuValArgTyr 140  
 QY 467 CATATGATAAATCCATATCTAATTAATTTAAGCAAAACCATGCTACTTTCTGATA 526  
 DB 141 HisMetIleLysHisProLysSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuLeu 160  
 QY 527 GCTACTGTCTGCACACTAGGTTTTCCTCATCTGTTTCCCTTCCAGTGTTCACAGTCTT 586  
 DB 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
 QY 587 GTGGAACTTCAAGAAACATTTGGTTGAGTGTGCTGAGCAGCAGGTATTATGTTGTCAG 646  
 DB 181 ValGluLeuGlnGluThrPheAspSerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200  
 QY 647 TCATGGCCATCTGATTTCATACAGAAATTCCTTACTATCTCTTTATTCAGTTCAGTAT 706  
 DB 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220  
 QY 707 ATTCGCCCTTAGTTTGTCTTACTGTAGTCTATACAGTGTCTGAGAGTATAGCTGT 766  
 DB 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
 QY 767 GGATTGTCCCAACAAAGAAACAGACTTGAAGAAATAGAGATGATCAACTTAACCTTTCAT 826  
 DB 241 GlyLeuSerAsnLysGluAsnLysLeuGluGluAsnGluMetIleAsnLeuThrLeuGln 260  
 QY 827 CCATCCAAAAGAGTGGGCTCAGGTGAAACTCTCTGGCAGCCATAAATGAGATTATCA 886  
 DB 261 ProPheLysLysSerGlyProGlnValLysLeuSerSerHisLysLysTrpSerTyrSer 280  
 QY 887 TTCATCAAAAACACAGAGAGATATAGCAAGAGACAGCATGTGTGTACCTGCTCCA 946  
 DB 281 PheIleArgLysHisArgArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
 QY 947 GAAAGACCTTCTCAAGAGAACCACTCCAGAAATACTCCAGAAAACCTTGGCTCTCTAAGA 1006



Db 48 ValAspSerLeuGlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPhe 67  
 QY 215 ATGGGAATCTACTATTATTTAATGGCTCTCATGAAAAAGCGTAATCAAGACATACGGTA 274  
 Db 68 MetGlyAsnLeuLeuIleValMetAlaValMetLysLysArgAsnGlnLysThrVal 87  
 QY 275 AACTTCCTCATAGGCAATCTGGCTTTTCTCATATCTTGGTTGGCTTTTGGCTCACT 334  
 Db 88 AsnPheLeuIleGlyAsnLeuAlaPheSerAspLeuValValPheCysSerPro 107  
 QY 335 TTCACACTGAGCTCTCTCTGATCAGTGGATGTTTGGCAAGATCTGTCATATT 394  
 Db 108 PheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGlyLysAlaMetCysHisIle 127  
 QY 395 ATGGCTTTCTCAATGCTGCTAGTTTGGTTTCACTTTAATTTAATATCAATGGCC 454  
 Db 128 MetProPheLeuGlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAla 147  
 QY 455 ATTGTGAGTATCATATAAAACATCCCATATCTAATATTAATTAACAGCAAAACCATGGC 514  
 Db 148 IleValArgTyrHisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGly 167  
 QY 515 TACTTTCTGATAGTCTGCTGACACTAGGTTTGGCTTCCATCTGTTCTCCCTTCCAGTG 574  
 Db 168 TyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProVal 187  
 QY 575 TTTCACAGCTCTGTGGAACTTCAAGAAACATTTGGTTGAGTCTGAGCAGCAGGTAT 634  
 Db 188 PheHisSerLeuValGluLeuLysGluThrPheGlySerAlaLeuLeuSerSerLysTyr 207  
 QY 635 TTATGTGTGAGTCATGCCATCTGATCATACAGAAATTCGTTTACTTCTTCTTATTG 694  
 Db 208 LeuCysValGluSerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeu 227  
 QY 695 CTAGTTCAGTATATCTGCCCTTAGTTGCTTACTGCTAGTACATACAGAGTCTGCAGA 754  
 Db 228 LeuValGlnTyrIleLeuProLeuValCysLeuThrValSerHisThrSerValCysArg 247  
 QY 755 AGTATAAGCTGTGGATTGTCCAAACAAAGAAACAGACTTGAAGAAATGAGATGATCAAC 814  
 Db 248 SerIleSerCysGlyLeuSerHisLysGluAsnArgLeuGluGluAsnGluMetIleAsn 267  
 QY 815 TTAACCTCTTCATCCATCAAAAGAGTGGGCTCAGGTGAACTCTCTGGCAGCCATAA 874  
 Db 268 LeuThrLeuGlnProSerLysLysSerArgAsnGlnAlaLysThrProSerThrGlnLys 287  
 QY 875 TGGAGTTATTCATTCATCAAAAGAGTGGGCTCAGGTGAACTCTACAGAGAGAGAGATG 934  
 Db 288 TrpSerTyrSerPheIleArgLysHisArgArgTyrSerLysLysThrAlaCysVal 307  
 QY 935 TTACTGTCTCAGAAAGACCTTCTCAGAGAACCACTCCAGATACTTCCAGAAACTTT 994  
 Db 308 LeuProAlaProAlaGlyProSerGlnGlyLysHisLeuAlaVal---ProGluAsnPro 326  
 QY 995 GGCTCTGTGAAGTTCAGCTCTCTTCATCAGTAGTAACTTACAGAGGGTCCCACTTGC 1054  
 Db 327 AlaSerValArgSerGlnLeuSerProSerSerLysValIleProGlyValProIleCys 346  
 QY 1055 TTTGAGATAAAACCTGAGAAATTCAGATGTTTCATGAATGAGAGTAAACGTTCTGTT 1114  
 Db 347 PheGluValLysProGluLysSerAspAlaHisGluMetArgValLysArgSerIle 366  
 QY 1115 ACAGNATAAAAGAGATCTGAGTCTTTTCTACAGATGAGCAGCTGATATATAGTA 1174  
 Db 367 ThrArgIleLysLysArgSerValPheLysArgLeuThrIleLeuIleLeuVal 386  
 QY 1175 TTTGCTGTGATGAGTCCACTACACTTTTCCATGTGTGTAATGTTTAAATGACAAT 1234  
 Db 387 PheAlaValSerTrpMetProLeuHisValPheHisValValThrAspPheAsnAspAsn 406  
 QY 1235 CTTATTTCAATAGCATTTCAAGTTGGTGTATGCAATTTGCTATTTGTTGGCAGTATG 1294  
 Db 407 LeuIleSerAsnArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMet 426

QY 1295 TCCTGTTCTTAATCAATCTATATATGGTTTCTTAATATGGATTAAGCTGATTTA 1354  
 Db 427 SerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnGlnGlyLysAlaAspLeu 446  
 QY 1355 GTGTCCTTATACACTGCTCTTCATATG 1381  
 Db 447 ArgAlaLeuIleHisCysLeuHisMet 455  
 RESULT 7  
 ID NY5R\_MOUSE STANDARD; PRT; 466 AA.  
 AC 070342; O35380; 09JMK1;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor).  
 DE Name=Npy5r; Synonyms=Npy5;  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99017379; PubMed=9802393;  
 RA Borowsky B., Walker M.W., Bard J., Weinshank R.L., Laz T.M., Vaysses P., Branchek T.A., Gerald C.;  
 RT "Molecular biology and pharmacology of multiple NPY Y5 receptor species homologs";  
 RL Regul. Pept. 75:45-53 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv; TISSUE=Brain;  
 RA Chen H., Adams S., McWhinnie E., Bayne M., Gadski R., Zastawny R.;  
 RT "Mouse neuropeptide Y Y5 receptor characterized by repeat sequence in extracellular domain";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97459646; PubMed=9315606; DOI=10.1016/S0005-2736(97)00131-4;  
 RA Nakamura M., Yokoyama M., Watanabe H., Matsumoto T.;  
 RT "Molecular cloning, organization and localization of the gene for the mouse neuropeptide Y-Y5 receptor";  
 RL Biochim. Biophys. Acta 1328:83-89 (1997).  
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylylate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Highest to tachykinins receptors.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; AF049329; AAC17839.1; -  
 CC EMBL; AF022948; AAB1829.1; -  
 CC EMBL; AB001346; BAA89538.1; -  
 CC GCD; MG1:108082; Npy5r.  
 CC GO; GO:0016020; C:membrane; IDA.  
 CC GO; GO:0001602; F:pancreatic polypeptide receptor activity; IDA.  
 CC GO; GO:0001601; F:peptide YY receptor activity; IDA.  
 CC GO; GO:0007273; P:regulation of synapse; IMP.  
 CC InterPro; IPR000276; GPCR\_Rhodpsn.  
 CC InterPro; IPR000393; NPY5\_receptor.  
 CC InterPro; IPR000811; NPY\_receptor.  
 CC Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PRO0237; GPCRHOOPS.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; FALSE\_NEG.  
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
KW Phosphorylation; Transmembrane.  
FT DOMAIN 1 61 Extracellular (Potential).  
FT TRANSMEM 62 83 1 (Potential).  
FT DOMAIN 84 95 Cyttoplasmic (Potential).  
FT TRANSMEM 96 116 2 (Potential).  
FT DOMAIN 117 136 Extracellular (Potential).  
FT TRANSMEM 137 158 3 (Potential).  
FT DOMAIN 159 178 Cyttoplasmic (Potential).  
FT TRANSMEM 179 199 4 (Potential).  
FT DOMAIN 200 231 Extracellular (Potential).  
FT TRANSMEM 232 253 5 (Potential).  
FT DOMAIN 254 388 Cytoplasmic (Potential).  
FT TRANSMEM 389 411 6 (Potential).  
FT DOMAIN 412 424 Extracellular (Potential).  
FT TRANSMEM 425 448 7 (Potential).  
FT DOMAIN 449 466 Cytoplasmic (Potential).  
FT DISULFID 135 219 By similarity.  
FT LIPID 462 462 S-palmitoyl cysteine (Potential).  
FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 17 17 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 39 39 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 195 195 L -> P (in Ref. 1).  
FT CONFLICT 284 284 K -> Q (in Ref. 3).  
SQ SEQUENCE 466 AA; 52784 MW; B157F236EF24385 CRC64;

Alignment Scores:  
Pred. No.: 2,8e-162 Length: 466  
Score: 2070.00 Matches: 397  
Percent Similarity: 90.13% Conservative: 23  
Best Local Similarity: 85.19% Mismatches: 24  
Query Match: 83.47% Indels: 22  
DB: 1 Gaps: 2

US-09-771-956-4 (1-1406) x NYSR\_MOUSE (1-466)

QY 47 ATGATTTAGAGTCGACGAGTATTATACAGACACTTCCACAGAGATATATCTGCT 106  
Db 1 MetGluValLysLeuGluHisPheAsnLysThrPheValThrGluAsnAsnThrAla 20  
QY 107 GCCACT----- 112  
Db 21 AlaSerGlnAsnThrAlaSerProAlaTrpGluAspTyrArgGlyThrGluAsnAsnThr 40  
QY 113 -----CGGAATCTGATTTCCAGTCTGGGATGACTATATAAGACAGTGTAGATGAC 163  
Db 41 SerAlaAlaArgAsnThrAlaPheProValTrpGluAspTyrArgGlySerValAspAsp 60  
QY 164 TTACAGTATTTTCGATGGGCTCTATACATTTGTAGTCTCTTGGCTTTATGGGGAAT 223  
Db 61 LeuGlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsn 80  
QY 224 CTACTTTATTTTATGGCTCTCATGAAAGAGCTAATCAGAGACTACGGTAAACTTCCTC 283  
Db 81 LeuLeuLeuLeuMetAlaValMetLysLysArgAsnGlnLysThrThrValAsnPheLeu 100  
QY 284 ATAGCAATCTGGCTTTTCGATATCTTGGTGTCTGCTGCTTTCCTCACCCTTCACACTG 343  
Db 101 IleGlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeu 120  
QY 344 ACGTCTGCTGCTGGATCAGTGTGATGTTGGCAAGTCTATGTCCTATATATGCTTTT 403  
Db 121 ThrSerValLeuLeuAspGlnTrpMetPheGlyLysAlaMetCysHisIleMetProPhe 140  
QY 404 CTTCAATGTGTCAGTTTGGTTTCAACTTTAATATATATCAATGTCATGTCAGG 463  
Db 141 LeuGlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArg 160  
QY 464 TATCATATGATAAACAATCCCATATCTAATATTTACAGCAACCATGGCTACTTCTG 523

161 TyrHisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeu 180  
524 ATAGTACTGTCTGGACACTAGGTTTTCGCCATCTGTTCCCTCCCTCCAGTGTTCACAGT 583  
181 IleAlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSer 200  
584 CTTGTGGAACCTTCAAGAAACATTTGGTTTCAGCATTTGCTGAGCAGCAGGATTTATGTGT 643  
201 LeuValGluLeuLysGluThrPheGlySerAlaLeuLeuSerSerLysTyrLeuCysVal 220  
644 GAGTCATGGCCATCTGATTCATACAGAAATTCCTTTACTATCTCTTTATGCTAGTTCAG 703  
221 GluSerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGln 240  
704 TATATTCGCCCTTAGTTTGTCTTACTGTAAGTCAATCAAGTGTCTCCAGAGATATAAGC 763  
241 TyrIleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSer 260  
764 TGTGATTTGTCACAAAGAAACAGACTTGAAGAAATGAGATGATCAACTTAACTCTT 823  
261 CysGlyLeuSerHisLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeu 280  
824 CATCCATCCAAAAAGAGTGGCCCTCAGGTGAACCTCTCTGGCAGCCATAAATGAGATAT 883  
281 HisProSerLysLysSerArgAspGlnAlaLysProProSerThrGlnLysTrpSerTyr 300  
884 TCATTTCATCAAAACACAGAGAGATATAGCAAGAGACAGCATGTCTGTTACTCTCT 943  
301 SerPheIleArgLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAla 320  
944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGATATCTCCAGAAACATTTGGTCTCTGTA 1003  
321 ProAlaGlyProSerGlnGluLysHisLeuThrVal---ProGluAsnProGlySerVal 339  
1004 AGAAGTCACTCTCTTCATCCAGTAAGTTCATACAGGGGTCCCCACTTGTCTTGAGATA 1063  
340 ArgSerGlnLeuSerProSerSerLysValIleProGlyValProIleCysPheGluVal 359  
1064 AAACCTGGAAGAAATTCAGATGTTTCATGAATTTGAGAGTAAACCTTCTGTTACAGAATA 1123  
360 LysProGluGluSerSerAspAlaGlnGluMetArgValLysArgSerLeuThrArgile 379  
1124 AAAAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTGATATAGTATTTGCTGCT 1183  
380 LysLysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuValPheAlaVal 399  
1184 AGTTGATGCCACTACACCTTTTCCATGTTGTAAGTAACTGATTTTAATGACAACTTTATTTCA 1243  
400 SerTrpMetProLeuHisValPheHisValThrAspPheAsnAspAsnLeuIleSer 419  
1244 AATAGGCATTTCAAGTGTGTTGATTCATTTGTCATTTGTTGGGCATGATGTCCTGTTGT 1303  
420 AsnArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCys 439  
1304 CTTATCCAACTCTATATGGTTCCTTAATATGGGATTAAGCTGATTAGTGTAGTCCCTT 1363  
440 LeuAsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuArgAlaLeu 459  
1364 ATACACTGCTCTCATATG 1381  
460 IleHisCysLeuHisMet 465

RESULT 8  
BAC32426 PRELIMINARY; PRT; 466 AA.  
ID BAC32426  
AC BAC32426  
DT 14-APR-2004 (rEMBLrel. 27, Created)  
DT 14-APR-2004 (rEMBLrel. 27, Last sequence update)  
DT 14-APR-2004 (rEMBLrel. 27, Last annotation update)  
DE Adult male corpora quadrigenina cDNA, RIKEN full-length enriched  
DE library, clone:B230213K17 product:NEUROPEPTIDE Y RECEPTOR TYPE 5, full  
DE insert sequence.



OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA THE FANTOM Consortium;

RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN (2)

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN (3)

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN (4)

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN (5)

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nishi K., Nagao S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Iwama M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN (6)

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanganaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK045587; BAC32426.1;  
 KW Neuropeptide; Receptor.  
 SQ SEQUENCE 466 AA; 52784 MW; B157F236EF2D4385 CRC64;

Alignment Scores:

Pred. No.: 2,8e-162 Length: 466

Score: 2070.00 Matches: 397

Percent Similarity: 90.13% Conservative: 23

Best Local Similarity: 85.19% Mismatches: 24  
 Query Match: 83.47% Indels: 22  
 DB: 2 Gaps: 2  
 US-09-771-956-4 (1-1406) x BAC32426 (1-466)  
 QY 47 ATGGATTAGACTCGACGAGTATTATAACAAGACACTTGCACAGAGAAATAACTGCT 106  
 Db 1 MetGluValLysLeuGluGluHisPheAsnLysThrPheValThrGluAsnAsnThrAla 20  
 QY 107 GCCACT----- 112  
 Db 21 AlaSerGlnAsnThrAlaSerProLalaTrpGluAspTyrArgGlyThrGluAsnAsnThr 40  
 QY 113 -----CGGAATTTCTGATTTCCCACTCTGGGAGTACTATAAAGCAGTGTAGATGAC 163  
 Db 41 SerAlaAlaArgAsnThrAlaPheProValTrpGluAspTyrArgGlySerValAspAsp 60  
 QY 164 TTACAGTATTTCTGATTTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGAAT 223  
 Db 61 LeuGlnTyrPheLeuLeuGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsn 80  
 QY 224 CTACTTATTTTAAATGGCTCTCATGAAAAGCGTAAATCAGAAAGACTACGCTAAACTTCCTC 283  
 Db 81 LeuLeuLeuLeuMetAlaValMetLysLysArgAsnGlnLysThrThrValAsnPheLeu 100  
 QY 284 ATAGCAATCTGGCCTTTCTGATATCTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 343  
 Db 101 IleGlyAsnLeuAlaPheSerAspIleLeuValLeuPhePheCysSerProPheThrLeu 120  
 QY 344 ACGTCTGCTTCTGCGATCAGTGGATGTTTGGCAAGGTCATGTCCTCATATTATGCTTTT 403  
 Db 121 ThrSerValLeuLeuAspGlnTrpMetPheGlyLysAlaMetCysHisIleMetProPhe 140  
 QY 404 CTTCAATGTGTGTCAGTTTGGTTTCAACTTAAATTTTAAATATATCAATTCGCAATGTG 463  
 Db 141 LeuGlnCysValSerValLeuValSerThrLeuIleLeuSerIleAlaIleValArg 160  
 QY 464 TATCATATGATAAACATCCCATATCTAATAATTAACAGCAACCATGCTACTTCTG 523  
 Db 161 TyrHisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeu 180  
 QY 524 ATAGTACTGTCTGGACACTAGTGTTCGCAATCTGTTCTCCCTTCCAGTGTTCACAGT 583  
 Db 181 IleAlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSer 200  
 QY 584 CTTGTGGAACCTCAAGAAACATTTGGTTCACCATGCTGACGACGAGTATTTATGTT 643  
 Db 201 LeuValGluLeuLysGluThrPheGlySerAlaLeuLeuSerSerLysTyrLeuCysVal 220  
 QY 644 GAGTCATGGCCATCTGATTCATACAGAAATTCCTTTTACTATCTCTTTATGCTAGTTT 703  
 Db 221 GluSerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGln 240  
 QY 704 TATATTCTGCCCTTAGTGTTCCTTACTGTAGTGCATACAAAGTGTCTGCAGAGTATAGC 763  
 Db 241 TyrIleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSer 260  
 QY 764 TGTGATTGTCCAAAGAAACAGACTTGAAGAAATCAGATGATGATCAACTTAACCTTT 823  
 Db 261 CysGlyLeuSerHisLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeu 280  
 QY 824 CATCCATCAAAAAGAGTGGGCTTCAGGTGAACCTCTCTGGCAGCCCAATAATGAGTTAT 883  
 Db 281 HisProSerLysLysSerArgAspGlnAlaLysProSerThrGlnLysTrpSerTyr 300  
 QY 884 TCATTTCATCAAAAACACAGAGAGATATAGCAGAGAGACAGCATGTGTGTTACCTGCT 943  
 Db 301 SerPheIleArgLysHisArgArgTyrSerLysThrAlaCysValLeuProAla 320  
 QY 944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGATATCTCCAGAAACTTTGGCTCTGTA 1003  
 Db 321 ProAlaGlyProSerGlnGluLysHisLeuThrVal---ProGluAsnProGlySerVal 339



QY 1004 AGAAGTCAGCTCTCTCATCCAGTAAGTTCATACCGGGTCCCACTGCTTGTGAGATA 1063  
 Db 340 AGSserGlnLeuSerProSerSerLysValleProGlyValProileCysPheGluVal 359  
 QY 1064 AAACCTGAAGAAATTCAGATGTTTCATGAATGAGAGTAAACGTTCTGTGTACAGATA 1123  
 Db 360 LysProGluGluSerSerAspAlaGlnGluMetArgVallyArgSerLeuThrArgile 379  
 QY 1124 AAAAGAGATCTCGAAGTGTTCCTACAGACTGCCATCTGATATAGTATTGCTGTT 1183  
 Db 380 LysLysAspGserArgSerValPheYrArgLeuThrIleLeuIleValPheAlaVal 399  
 QY 1184 AGTTGATGCCACTACACTTCCATGCTGTAATGTTTAAATGACAACTTATTTC 1243  
 Db 400 SerTrpMetProLeuHisValPheHisValThrAspPheAsnAspLeuIleSer 419  
 QY 1244 ATAGGCAATTCAGCTGGTGTATGTCATTTGTCATTTGTTGGCAGTGTCTGTTGT 1303  
 Db 420 AsnArgHisPheLysLeuValYrCysIleCysHisLeuLeuGlyMetSerCysCys 439  
 QY 1304 CTTAATCCAAATCTATATGGGTTTCTTAATATGGGATTAAGCTGATTTAGTGTCCCTT 1363  
 Db 440 LeuAsnProIleLeuYrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuArgAlaLeu 459  
 QY 1364 ATACACTGCTTCATATG 1381  
 Db 460 IleHisCysLeuHisMet 465

RESULT 9  
 NY5R\_PIG  
 ID NY5R\_PIG STANDARD; PRT; 446 AA.  
 AC O97959;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor).  
 DE receptor).  
 GN Name=NPY5R; Synonyms=NPYR5;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wraith A., Tornsten A., Chardon P., Harbitz I., Chowdhary B.P., Andersson L., Lathammar D.;  
 RT "porcine NPY receptors NPY1R, NPY2R and NPY5R: cloning, mapping and comparative analysis.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LWD; TISSUE=Kidney;  
 RA Ito Y., Minezawa M.;  
 RT "Sus scrofa gene for neuropeptide Y receptor type 5, complete cds.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylyate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Highest to tachykinins receptors.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF106093; AAD13778.1; -

DR EMBL; AB019185; BAA34055.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR000393; NPY5\_receptor.  
 DR InterPro; IPR000611; NPY\_receptor.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPS.  
 DR PROSITE; PS00237; G-PROTEIN RECF F1\_1; FALSE\_NEG.  
 DR PROSITE; PS0262; G-PROTEIN RECF F1\_2; 1.  
 DR G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
 KW Phosphorylation; Transmembrane.  
 KW DOMAIN 1 40 Extracellular (Potential).  
 FT TRANSMEM 41 62 1 (Potential).  
 FT DOMAIN 63 74 Cytoplasmic (Potential).  
 FT TRANSMEM 75 95 2 (Potential).  
 FT DOMAIN 96 115 Extracellular (Potential).  
 FT TRANSMEM 116 137 3 (Potential).  
 FT DOMAIN 138 157 Cytoplasmic (Potential).  
 FT TRANSMEM 158 178 4 (Potential).  
 FT DOMAIN 179 210 Extracellular (Potential).  
 FT TRANSMEM 211 232 5 (Potential).  
 FT DOMAIN 233 368 Cytoplasmic (Potential).  
 FT TRANSMEM 369 391 6 (Potential).  
 FT DOMAIN 392 404 Extracellular (Potential).  
 FT TRANSMEM 405 428 7 (Potential).  
 FT DOMAIN 429 446 Cytoplasmic (Potential).  
 FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 17 17 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 114 198 By similarity.  
 FT LIPID 442 442 S-palmitoyl cysteine (Potential).  
 SQ SEQUENCE 446 AA; 50474 MW; B7F616C394C6CA0 CRC64;

Alignment Scores:  
 Pred. No.: 8,24e-159 Length: 446  
 Score: 2028.00 Matches: 380  
 Percent Similarity: 93.03% Conservative: 34  
 Best Local Similarity: 85.39% Mismatches: 31  
 Query Match: 81.77% Indels: 0  
 DB: 1 Gaps: 0

US-09-771-956-4 (1-1406) X NY5R\_PIG (1-446)

QY 47 ATGATTTAGAGCTCGAGAGTATTATAACAAGACACTGCCACAGAGATAATATCTGCT 106  
 Db 1 MetGlySerGluIleProAspTyrTyrAsnLysThrLeuAlaSerGluAsnAsnThrVal 20  
 QY 107 GCACCTCGGAATTCGTATTCCTCCAGTCTGGGATGATCACTATAAAGACAGTGTAGATGACTTA 166  
 Db 21 AlaThrArgAsnSerGlyPheProValTrpGluAspTyrLysGlySerValAspAspLeu 40  
 QY 167 CAGTATTTCTGATGGGCTCTATACATTTGTAGTCTTCTGGCTTTATGGGGAATCTA 226  
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 QY 227 CTTATTTTAAATGGCTCTCATGAAAACGCGTAATCAGAAGACTACGGTAAACTTCCTCATA 286  
 Db 61 LeuLeuLeuMetAlaValMetArgLysArgAsnGlnLysThrThrValAsnPheLeuIle 80  
 QY 287 GCGAATCTGGCTTTCTCGATATCTTGGTGTGCTGTGTTGCTACCTTTACACATGACG 346  
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100  
 QY 347 TCTGTCTTCTGGGATCAGTGGATGCTTTGGCAAGTCTATGTGCCATATTATGCTCTTCTT 406  
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120  
 QY 407 CAATGTGTGTCAGTTTGGTTTCAACTTAAATTTTAAATATCAATGCCATGTGTCAGTAT 466  
 Db 121 GlnCysValThrValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140  
 QY 467 CATATGATAAACATCCCATATCTTAATAATTTAACAGCAACCATGGCTACTTCTTGATA 526  
 Db 141 HisMetIleLysHisProValSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160

QY 527 GCTACTGCTGCAGACTAGGTTTGGCCATCTGTTCTCCCTTCAGTGTTCACAGTCTT 586  
 Db 161 AlathrValTrpThrLeuGluAlaIleCysSerProLeuProValPheHisSerLeu 180  
 QY 587 GTGAACCTTCAAGAACATTTGGTTTGGCCATCTGTTCTCCCTTCAGTGTTCACAGTCTT 646  
 Db 181 ValGluLeuGlnGluSerPheGlySerAlaTrpLeuSerSerArgTyrLeuCysValGlu 200  
 QY 647 TCATGGCCATCTGATTCATACAGAAATGCTTACTATCTCTTATTCAGTGTTCACAGTCTT 706  
 Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220  
 QY 707 ATTCTGCTTACTGTTTCTTACTGTTAGTGCATCAAGTCTGTCAGAGTGTTCACAGTGTTC 766  
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgThrIleSerCys 240  
 QY 767 GGATGTCCAAACAAAGAAACAGACTTGAAGAAATGAGATGATCAACTTAACTTTCAT 826  
 Db 241 GlyLeuSerSerGlnAspSerLysLeuGluGluAsnGluMetIleAsnLeuThrLeuGln 260  
 QY 827 CCATCCAAAAGAGTGGCCCTCAGTGAACCTCTCTGGCAGCCATAAATGAGTATTCA 886  
 Db 261 ProAlaLysArgSerGlyProGlnAlaLysLeuSerHisHisProLysTrpThrTyrSer 280  
 QY 887 TTCATCAAAAACACAGAAAGATATAGCAAGAGACAGCATGTGTGTACCTGCTCCA 946  
 Db 281 PheIleArgArgHisArgTyrSerLysLysThrAlaCysValArgProAlaPro 300  
 QY 947 GAAAGACCTTCTCAAGAGAACCTCAGATATCTCCAGAAACCTTGGCTCTGTAGA 1006  
 Db 301 AlaGlyProAlaLeuLysArgGluGlyArgProGlyLysValGlySerMetGln 320  
 QY 1007 AGTCAGCTCTCTTCATCAGTAAGTTCATACAGAGGCTGCCACTTGTCTTGTAGATAAAA 1066  
 Db 321 SerGlnProProSerAsnLysPheMetProGlyValProThrCysPheGluValLys 340  
 QY 1067 CCTGAAGAAATTCAGATGTTTCAAGATGAGTAAACAGTCTGTCTGTACAAAGATAAAA 1126  
 Db 341 ProGluLysSerAspValProGluMetArgValSerArgSerIleMetArgLeuArg 360  
 QY 1127 AAGAGATCTCGAAGTGTCTTCTCAGATCAGTACCATCTGATATAGTATGCTGTACT 1186  
 Db 361 LysArgSerArgSerValPheTyrArgLeuThrValLeuIleLeuValPheAlaValSer 380  
 QY 1187 TGGATGCCACTACACCTTTCCATGTGGTAACATGATTTAATGACATCTTATTTCAAAT 1246  
 Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400  
 QY 1247 AGCATTTCAAGTGGTGTATTCGATTCATTTGTCATTTGTTGGCATGATGCTGTGCTTT 1306  
 Db 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuGlyMetMetSerCysLeu 420  
 QY 1307 AATCCAAATCTATATGGTTTCTTATATGGAATTAAGCTGATTTAGTGTCCCTTATA 1366  
 Db 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuMetSerLeuIle 440  
 QY 1367 CACTGCTTCAATG 1381  
 Db 441 HisCysLeuHisVal 445

RESULT 10

Q8QFM2 ID Q8QFM2 PRELIMINARY; PRT; 443 AA.  
 AC Q8QFM2  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DE Neurotrophin-4 (NT-4)  
 DE Neurotrophin-4 (NT-4)  
 DE Gallus gallus (Chicken)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;

RN SEQUENCE FROM N.A.  
 RP Holmberg S.K.S., Mikko S., Boswell T., Zoorob R., Larhammar D.;  
 RT "Pharmacological characterization of cloned chicken neurotrophin-4  
 receptors V1 and V5";  
 RL J. Neurochem. 0:0-0(2003).  
 DR EMBL; AY04844; AAK8356.1; --  
 DR GO; GO:0016021; C:intracellular to membrane; IEA.  
 DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.  
 DR InterPro; IPR000376; GPCR\_Rhodopsn.  
 DR InterPro; IPR000393; NPY5\_receptor.  
 DR InterPro; IPR000611; NPY5\_receptor.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PRO0237; GPCR\_Rhodopsn.  
 DR PRINTS; PRO1016; NRPEPTIDEVSR.  
 DR PRINTS; PRO1012; NRPEPTIDEVSR.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECIP\_F1\_2; 1.  
 DR Neurotrophin-4 Receptor.  
 SQ SEQUENCE 443 AA; 50044 MW; EPE9FIA391CC092E CRC64;

Alignment Scores:

Pred. No.: 6,778-126 Length: 443  
 Score: 1629.50 Matches: 310  
 Percent Similarity: 81.49% Conservative: 51  
 Best Local Similarity: 69.99% Mismatches: 77  
 Query Match: 65.71% Indels: 5  
 DB: 2 Gaps: 4

US-09-771-956-4 (1-1406) x Q8QFM2 (1-443)

QY 47 ATGNTTTAGAGTCTGCAGCATATATTAACAAGACACTTGCACAGAGATAAATCTGCT 106  
 Db 1 MetAspLeuGlyPheLysAspTyrThrAsnArgThr---ProThrLysAsnThrSerAla 19  
 QY 107 GCACCTCGAATCTGATTTCCTCCAGTCTGGCATCACTATAAAGCAGTGTAGATGACTTA 166  
 Db 20 ThrThrLysAsn-----PheSerAlaTrpGluAspTyrLysSerSerValAspAspIle 37  
 QY 167 CAGTATTTCTGATGGCTCTATACATTTGTAGTCTTCTTGTGCTTTATGGGAAATCTA 226  
 Db 38 GlnTyrPheLeuIleGlyLeuTyrThrLeuIleSerLeuAlaGlyPheValGlyAsnLeu 57  
 QY 227 CTTATTTTAAAGGCTCTCATGAAAAGCGTAATCAGAAAGACTACGGTAAACTTCTCAT 286  
 Db 58 LeuValLeuThrAlaLeu---ThrLysArgLysGlnLysThrIleIleAsnIleLeuIle 76  
 QY 287 GGCAATCTGGCTTTTCTGATATCTGTTGTGTGTTGCTGCTTACCTTTACACTGACG 346  
 Db 77 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 96  
 QY 347 TCTGCTTGTGGATCAGTGGATGTTTGGCAAGTCAATGTCATATATGCTTATGCTTTCTT 406  
 Db 97 SerValLeuLeuAspArgTrpMetPheGlyThrValMetCysHisIleMetProPheLeu 116  
 QY 407 CAATGTGTGTCAGTGTGTTTCAACTTTAATTTAATATCAATTTGCTTGTGCTGCTAT 466  
 Db 117 GlnCysThrSerValLeuValSerThrLeuMetLeuIleSerIleAlaAlaValArgTyr 136  
 QY 467 CATATGATAAATCCCATATCTAATAATTAACACAAACCATGCTACTTCTTGATA 526  
 Db 137 ArgMetValLysTyrProLeuSerSerAsnLeuThrAlaLysHisGlyTyrPheLeuIle 156  
 QY 527 GCTACTGCTGGACACTAGTGTGTTGGCATCTGTTCTCCCTTCCAGTGTTCACAGTCTT 586  
 Db 157 ValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 176  
 QY 587 GTGAACCTTCAAGAACTTGTGTTGCTGAGCATTCCTGAGCAGCAGGATTTATGTTGAG 646  
 Db 177 ValAspLeuHisLysThrLeuAsnLeuGluAlaLeuGluAsnArgLeuLeuCysIleGlu 196

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QY 647 TCATGCCCATCTGATTTCATACAGAAATGGCTTTACTATCTCTTTATGCTAGTCTAGTAT 706
Db 197 SerTyrProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuMetGlnTyr 216
QY 707 ATTCTGCCCTTACTGTTCTTACTGTAAGTCATACAGAGTGTCTGCAGAGTATAAGCTGT 766
Db 217 IleLeuProLeuValCysLeuThrAlaSerHisThrSerValCysArgSerValGlySer 236
QY 767 GGATTGTCACAAAGAAACACAGACTTGGAAGAAATGAGATGATCAACTTAACTCTTCAT 826
Db 237 ArgLeuSerSerLysGluGlyPheGlnGluAsnGluMetIleAsnLeuThrLeuHis 256
QY 827 CCATCCAAAAGAGTGGGCTCAGGTCAAACTCTCTGGCAGCCATAAATGGAGTTATCCA 886
Db 257 ProSerLysSerAlaGlyThrGluAlaGlnProSerSerHisThrSerTyrSerCysAla 276
QY 887 TCCATCAAAAACACAGAAAGATATAGCAAGAACACAGCATGTGTGTACTCTGCTCCA 946
Db 277 LeuValArgLysHisArgGlySerLysThrSerThrValMetProAlaIle 296
QY 947 GAAAGACCTTCTCAAGAGAACCTCCAGATACTCCAGAAACCTTGGCTCTGTAAAGA 1006
Db 297 LeuArgGlnGlnGlnAspAlaAspPheArgAspLeuProGluThrSerGlyThrGluLys 316
QY 1007 AGTCAGCTCTCTTCATCCAGTAAGTTCATACAGGGGTCCCACTTGCTTTGAGATAAAA 1066
Db 317 SerGlnLeuSerSerSerSerLysPheIleProGlyValProIleCysPheGluMetLys 336
QY 1067 CCTGAAGAAATTCAGATGTCATGAA---TTGAGAGTAAACGTTCTGTTCACAGAAATA 1123
Db 337 ProGluGluAsnThrGluIleGlnAspMetIleThrValSerGlnSerIleIleArgIle 356
QY 1124 AAAAGAGATCTCGAAGTGTCTTACAGACTGACCATCTGATATATAGTATTTGCTGTT 1183
Db 357 LysThrArgSerArgArgValPheCysArgLeuThrValLeuLeuValPheGlyPhe 376
QY 1184 AGTTGATGTCACATACACCTTTTCCATGTGTGTAAGTATTTAATGACAACTTATTTCA 1243
Db 377 SerTyrMetProLeuHisLeuPheHisIleValThrAspPheAsnAlaThrLeuIleSer 396
QY 1244 AATAGGCAATTCAGTTGGTGTATGCTATTTGTCATTTGTTGGCATGATGCTCTGTGT 1303
Db 397 AsnArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetSerCysCys 416
QY 1304 CTTAATCCAACTCATATGGTTTCTTAATAATGGGATTAAGCTGATTTAGTGTCCCTT 1363
Db 417 LeuAsnProIleLeuTyrGlyPheLeuAsnAsnSerIleLysAlaAspLeuMetSerLeu 436
QY 1364 ATACACTGT 1372
Db 437 IleProCys 439

RESULT 11
ID O73733 PRELIMINARY; PRT; 377 AA.
AC O73733;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neuropeptide Y/peptide YY receptor Ya.
GN Name=NPYr; Synonyms=NPYrYA; (Danio rerio).
OS Brachydanio rerio (Zebrafish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98068942; PubMed=9407007;
RA Lundell I., Berglund M.M., Starback P., Salaneck B., Gehlert D.R.,
RA Larhammar D.;
RT "Cloning and characterization of a novel neuropeptide Y receptor
RT subtype in the zebrafish."
```

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RL DNA Cell Biol. 16:1357-1363(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98096393; PubMed=9434780;
RA Ringvall M., Berglund M.M., Larhammar D.;
RA "Multiplicity of neuropeptide Y receptors: cloning of a third distinct
RT subtype in the zebrafish."
RT Biochem. Biophys. Res. Commun. 241:749-755(1997).
RL [3]
RN SEQUENCE FROM N.A.
RP MEDLINE=99337783;
RA Starback P., Lundell I., Fredriksson R., Berglund M.M., Yan Y.L.,
RA Wraath A., Soderberg C., Postlethwait J.H., Larhammar D.;
RA "Neuropeptide Y receptor subtype with unique properties cloned in the
RT zebrafish: the zY receptor."
RL Brain Res. Mol. Brain Res. 70:242-252(1999).
DR EMBL; AF037400; AAC41276.1; -.
DR ZFIN; ZDB-GENE-980526-393; npyrya.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000351; NPYL_receptor.
DR InterPro; IPR000611; NPY_receptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01013; NRPEPTIDEYR.
DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; UNKNOWN 1.
DR PROSITE; PS0262; G_PROTEIN_RECPEP_F1_2; 1.
DR KW Neuropeptide; Receptor.
SQ SEQUENCE 377 AA; 42901 MW; 60B62AD9C7BF5D0 CRC64;

Alignment Scores:
Pred. No.: 2,148-37 Length: 377
Score: 558.00 Matches: 124
Percent Similarity: 44.24% Conservative: 68
Best Local Similarity: 28.57% Mismatches: 136
Query Match: 22.50% Indels: 106
DB: 2 Gaps: 6

US-09-771-956-4 (1-1406) x O73733 (1-377)
QY 74 AACAAAGACACTTCCACAGAGAAATAATCTGCTGCCACTCGGAATCTGATTCCTCAGTC 133
Db 16 AsnSerThrLeuThrHisAsnGlnSerAsnSerSerLeuPheLeuLeuAspValProCys 35
QY 134 TGGGATGACTATAAAGACGAGTGTAGTACCTTACAGTATTTCTGATTTGGGCTCTATACA 193
Db 36 Trp-----GlnSerSerThrMetThrLeuThr-----LeuValLeuCysTyrCys 50
QY 194 TTGTGAAGTCTTCTGGCTTTATGGGAATCTACTTATTTAATGGCTCTCATGAAAAG 253
Db 51 LeuValLeuLeuLeuGlyLeuLeuGlyAsnIleLeuLeuIleCysIleIleMethHisGln 70
QY 254 CGTAATCAGAAGACTACGGTAAACTTCTCATAGCAATCTGCCCTTTCTGATATCTTG 313
Db 71 ArgAspProProAsnValThrSerIleLeuIleAlaAsnLeuSerValSerAspIleLeu 90
QY 314 GTTGTGCTGTTTGTGCTCACCTTTTCACACTGACGCTGTCTTGTGTCAGTCAGTGTGT 373
Db 91 ValSerValPheCysLeuProPheThrValValTyrThrLeuMetAspHisIlePhe 110
QY 374 GGCAAGTCATGTGCCATATATATGCTTTTCTTCAATGTGTGTGTCAGTTTGGTTCAACT 433
Db 111 GlyAlaLeuLeuCysArgLeuMetProPheValGlnCysValSerValThrValSerVal 130
QY 434 TTATTTTATATCAATTCCTGCTTGTTCAGTATCATATGATATAAACAATCCCATATCTAAT 493
Db 131 LeuSerLeuValLeuLeuAlaLeuGluArgHisGlnLeuLeuLeuHisProSerGlyTrp 150
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QY 494 AATTAAACAGCAAAACCATGGCTACTTTCTGATAGCTACTGCTCGACACTAGGTTTGGCC 553  
 Db : : : : :  
 151 LysProSerValProGlnAlaTyrIleAlaValLeuThrValTrpLeuLeuAlaCysVal 170  
 QY 554 ATCTGTTCTCCCTCCAGTGTTCACAGTCTTGTGGACCTTCAAGAAACATTTGGTTCA 613  
 Db : : : : :  
 171 ThrSerLeuProPheLeuAlaPheHisLeuLeuThrSerGluProTyrSerLeuPhePro 190  
 QY 614 GCATTGCTGACAGCAGGATATTATGTTGAGTCATGGCCATCTGATTCATACAGAAATT 673  
 Db : : : : :  
 191 AlaProLeuSerGlnLeuGlnValCysLeuGluValTrpProSerGlnAspHisLysLeu 210  
 QY 674 GCCTTTACTATCTCTTATCTGCTAGTTCAGTATATCTGCTTGTGCTTGTCTTACTGTA 733  
 Db : : : : :  
 211 AlaTyrThrThrSerLeuLeuPheGlnTyrCysCysProLeuLeuMetLeuLeu 230  
 QY 734 AGTCATACAAGTGTCTGCAGAAATAGTGTGATTTGTCATCCAAACAAAGAAACAGACTT 793  
 Db : : : : :  
 231 CystyrLeuArgIle----- 235  
 QY 794 GAAGAAATGAGATGATCACTTAACCTTCATCCATCCAAAGAGAGTGGCCCTCAGGTG 853  
 Db : : : : :  
 235 ----- 235  
 QY 854 AAACCTCTGCGCAGCCATAATGAGTTATTTCATTCATCAAAAACACAGAAGATAT 913  
 Db : : : : :  
 236 -----PheLeuArgLeuGlnArgGluArg 244  
 QY 914 AGCAAGAGACAGCATGTGTGTTTACCTGCTCAGAAAGACCTTCTCAAGAGAACCCTCC 973  
 Db : : : : :  
 245 MetLeuGluArgGlnCys-----SerArgAsnArgGluAspGluHisArg 259  
 QY 974 AGATACTTCAGAAAACCTTTGGCTCTGTAAGAGTCAGCTCTCTTCATCCAGTAAGTTC 1033  
 Db : : : : :  
 260 ArgValMet----- 262  
 QY 1034 ATACCAGGGTCCCACTTCTGTTGAGATAAAACCTGAAGAAATTCAGATGTTTCATGAA 1093  
 Db : : : : :  
 262 ----- 262  
 QY 1094 TTGAGAGTAAACCTTCTGTTACAGAAATAAAGAGATCTCGAAGTGTTCACAGA 1153  
 Db : : : : :  
 263 -----HisSerLysArgIleAsnValMet 270  
 QY 1154 CTGACCATCTGATATTAGTATTGCTGTTAGTGGATGCCACTACACCTTTTCCATGTG 1213  
 Db : : : : :  
 271 LeuAlaThrLeuValAlaAlaPheAlaValCysTrpLeuProLeuAsnAlaPheAsnVal 290  
 QY 1214 GTAACCTATTTAATGACATCTTATTTCATAAGGCAATTCAGTTGGTGTGATTCGATT 1273  
 Db : : : : :  
 291 ValAlaAspCysAspGlnGluValLeuProValCysAsnHisAsnLeuLeuPheSerLeu 310  
 QY 1274 TGTCATTTGTTGGCAGTGTCTGTTGCTTAACTCAATCTCTATATGGGTTCTTAAT 1333  
 Db : : : : :  
 311 CysHisLeuLeuAlaMetSerThrCysValAsnProIleIleIleIleIleIleIleIle 330  
 QY 1334 AATGGGATTAAAGCTGATTAGTGTCCCTTATA---CACTGT 1372  
 Db : : : : :  
 331 SerAsnPheArgLysAspValAlaSerValValLeuHisCys 344

## RESULT 12

Q6Y6A4 ID Q6Y6A4 PRELIMINARY; PRT; 348 AA.  
 AC Q6Y6A4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE NPX receptor Y1 (Fragment).  
 OS Squalus acanthias (spiny dogfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Hypnosqualea; Squaliformes; Squaloidae;  
 OC Squalidae; Squalus.  
 CX NCBI\_TaxID=7797;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=22763539; PubMed=12777532;  
 RA Salaneck E., Ardehl D.H., Larson E.T., Lathammar D.;  
 RT "Three neuropeptide X receptor genes in the spiny dogfish, Squalus  
 acanthias, support en bloc duplications in early vertebrate  
 evolution."; Mol. Biol. Evol. 20:1271-1280(2003).  
 RL [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Salaneck E.W., Larson E.T., Ardehl D.H., Lathammar D.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AY177273; AAO62565.1; -.  
 DR EMBL; AY177273; AAO62565.1; JOINED.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR000351; NPX\_receptor.  
 DR InterPro; IPR000611; NPX\_receptor.  
 DR Pfam; PF00001; 7tm1; 1.  
 DR PRINTS; PRO0237; GPCR\_RHODOPSIN.  
 DR PRINTS; PRO1013; NRPEPTIDEYR.  
 DR PRINTS; PRO1012; NRPEPTIDEYR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 FT NON\_TER 348  
 SQ SEQUENCE 348 AA; 40738 MW; 817D35C53DAFD90F CRC64;

## Alignment Scores:

Pred. No.: 7, 73e-35 Length: 348  
 Score: 527.00 Matches: 115  
 Percent Similarity: 43.30% Conservative: 79  
 Best Local Similarity: 25.67% Mismatches: 122  
 Query Match: 21.25% Indels: 132  
 DB: 2 Gaps: 7

US-09-771-956-4 (1-1406) x Q6Y6A4 (1-348)

QY 29 TCACAGAGAGACTATATATATGATTTAGCTGACGAGTATTATACAGACACTTGGCC 88  
 Db : : : : :  
 19 SerGluArgAsnPheThrLeuAsp---AsnTyrAspGlnCysTyrSerGlnThrAla--- 36  
 QY 89 ACAGAGATAATACTGCTGCCACTCGGAATTCGTATTCGCCAGTCTGGGAGACTATAAA 148  
 Db : : : : :  
 36 ----- 36  
 QY 149 AGCAGTGTAGAGACTTACAGTATTTCTGATTTGGCTCTATACATTGTGAAGTCTCTT 208  
 Db : : : : :  
 37 -----MetIlePheThrLeuAlaLeuIleTyrSerAlaIleLeu 51  
 QY 209 GGCITTTATGGGAATCTACTTTATTTAATGCTCTCATGAAAAGCGTAATCAGAGACT 268  
 Db : : : : :  
 52 GlyValSerGlyAsnLeuLeuIleThrIleIleMetLysGlnLysGluMetHisAsn 71  
 QY 269 ACGGTAACCTCTCTCATAGGCAATCTGGCTTTTCTGATATCTTGGTGTGCTCTTTGC 328  
 Db : : : : :  
 72 ValThrAsnIleLeuIleValAsnLeuSerValSerAspLeuLeuIleSerValMetCys 91  
 QY 329 TCACCTTTACAGTACGCTCTGCTGCTGCTGATGAGTGTGTTGGCAAGTCAATCTGC 388  
 Db : : : : :  
 92 LeuProPheThrLeuValTyrThrPheMetAspHisIleIlePheGlyGluAlaMetCys 111  
 QY 389 CATATTATGCTCTTTCTCAATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 448  
 Db : : : : :  
 112 LysLeuAsnSerMetIleGlnCysIleSerIleThrValSerIlePheSerLeuValLeu 131  
 QY 449 ATTGCCATTGTCAGTATCATATGATAAATCCCATATCTAATTAATTAATATCA 508  
 Db : : : : :  
 132 IleAlaValGluArgHisGlnLeuIleAsnProGlnGlyTyrArgProAsnAsnLys 151  
 QY 509 CATGCTACTTCTGTAGTACTGTCTGAGACACTAGGTTTGGCATCTGCTTCCCTCTT 568

Db 152 HisAlaTyrLeuSerIleValThrMetTyrThrLeuAlaLeuLeuThrSerLeuProPhe 171  
QY 569 CCAGTGTTCACAGTCTGTGGAACTTCAAGAAACATTTGGT---TCACATGTCGTGAC 625  
Db 172 LeuLeuPheHisAsnLeuThrAspGluGlnPheHisGlyTyrSerThrGluPheAla 191  
QY 626 AGCAGTATTATGCTGTGAGTCATGCCATCTGATTCATACAGAAATTCCTTTACTATC 685  
Db 192 GlyLysTyrMetCysLeuGluGlnTyrProSerGluThrGluArgLeuValTyrThr 211  
QY 686 TCTTTATGCTAGTTCAGTATATCTGCGCTTGTAGTTTGTCTTACTGTAAGTACATCAAGT 745  
Db 212 CysLeuLeuValMetGlnTyrPheAlaProLeuCysPheIlePheIleCysTyrPheLys 231  
QY 746 GTCGTGAGAGTATAGCTGTGATGTCCTCAACAAAGAAACACAGACTTCAAGAAATGAG 805  
Db 232 Ile----- 232  
QY 806 ATGATCAACTTAATCTCTTCATCCATCAAAAGAGTGGGCTCAGGTGAACCTCTCTGCG 865  
Db 232 ----- 232  
QY 866 AGCCATAATGGAGTTATTCAATTCATCAAAACACAGAAAGATATAGCAAGAGACA 925  
Db 233 -----TyrIleArgLeuArgArgAsnAsnThrMet----- 243  
QY 926 GCAATGCTGTACTGCTGCAGAAAGACCTTCTCAAGAGAACCACTCCAGAAATACTTCCA 985  
Db 244 -----AspLysMetArgGluGluAsn----- 250  
QY 986 GAAAACTTTGGCTCTGTAAGAGTCACTCTCTTCATCCAGTAAGTTCATACACGGGGTC 1045  
Db 250 ----- 250  
QY 1046 CCCACTTGTCTTGAGATAAACCTGAGAAATTCAGATGTTTCATGAATGAGAGTAAAA 1105  
Db 251 -----LysTyrArgAlaAspGluAsn----- 257  
QY 1106 CGTCTGTTCAAGATAAAAGAGATCTCGAAGTGTTTTCACAGACTGACCATCTG 1165  
Db 258 -----ArgArgIleAsnIleMetLeuIleSerIle 267  
QY 1166 ATATTAGTATTGCTGTAGTGTGATGCCACTACCTTCCATGTTGTAAGTATTT 1225  
Db 268 ValValAlaPheAlaIleCysTyrLeuProLeuAsnIlePheAsnAlaValPheAspTyr 287  
QY 1226 AATGACAATCTTATTTCAAATAGGCATTTCGAAGTTGGTGTATTCGATTTGCTTTGTTG 1285  
Db 288 AsnTyrGluValIleAsnAsnCysHisAsnLeuValPheSerIleCysHisLeuThr 307  
QY 1286 GGCATGATGCTGCTGTTGTTTAAATCCAAATTCATATGCGTTTCTTAATATGGAATAA 1345  
Db 308 AlaMetLeuSerThrCysThrAsnProIlePheTyrGlyPheLeuAsnLysAsnPheGln 327  
QY 1346 GCTGATTTAGTGTCCCTTATACAC 1369  
Db 328 ArgAspLeuArgSerIleLeuHis 335  
RESULT 13  
AAO62565  
ID AAO62565 PRELIMINARY; PRT; 348 AA.  
AC AAO62565;  
DT 25-MAR-2004 (TrEMBLrel. 27, Created)  
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE NPY receptor v1 (Fragment).  
OS Squalus acanthias (Spiny dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.  
OX NCBI\_TaxID=7797;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=22763539; PubMed=12777532;  
RA Salaneck E., Ardell D.H., Larson E.T., Larhammar D.;  
RT "Three Neuroptide Y Receptor Genes in the Spiny Dogfish, Squalus  
RT acanthias. Support en Bloc Duplications in Early Vertebrate  
RL Mol. Biol. Evol. 20:1271-1280(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Salaneck E.W., Larson E.T., Ardell D.H., Larhammar D.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY177273; AAO62565.1; -  
DR EMBL; AY177272; AAO62565.1; JOINED.  
KW Receptor.  
FT NON TER 348 348  
SQ SEQUENCE 348 AA; 40738 MW; 817D35C53DAFD90F CRC64;  
Alignment Scores:  
Pred. No.: 7, 73e-35 Length: 348  
Score: 527.00 Matches: 115  
Percent Similarity: 43.30% Conservative: 79  
Best Local Similarity: 25.67% Mismatches: 122  
Query Match: 21.25% Indels: 132  
DB: 2 Gaps: 7  
US-09-771-956-4 (1-1406) X AAO62565 (1-348)  
QY 29 TCCAAAGCAGGACTATAATATGATTCAGCTCGACGAGTATTATACACAGACACTTCC 88  
Db 19 SerGluArgAsnPheThrLeuAsp---AsnTyrAspGlnCysTyrSerGlnIleAla--- 36  
QY 89 ACAGAGAATAATACTGCTGCCACTCGGAATTCGATTTCCAGTCTGGGATGACTATAAA 148  
Db 36 ----- 36  
QY 149 AGCAGTGTAGTACTACAGTATTTCTGATGCGCTCTATACATTTGTAGTCTTCTT 208  
Db 37 -----MetIlePheThrLeuAlaLeuIleTyrSerAlaIleIleLeu 51  
QY 209 GCGTTTATGGGAATCTACTTATTTAATGCTCTCATGAAAAAGCGTAATCAGAAAGCT 268  
Db 52 GlyValSerGlyAsnLeuLeuIleThrIleMetLysGlnLysGluMetHisAsn 71  
QY 269 ACGGTAACCTTCTCATAGCAATCTGCGCTTTCTGATATCTTGGTGTGCTGTTTGC 328  
Db 72 ValThrAsnIleLeuIleValAsnLeuSerValSerAspLeuIleSerValMetCys 91  
QY 329 TCACCTTTCACACTGACGCTCTCTTGTGGATCAGTGTGATCTTTGGCAAGTCAATGTC 388  
Db 92 LeuProPheThrLeuValTyrThrPheMetAspHisTyrIlePheGlyGluAlaMetCys 111  
QY 389 CATATTATGCTTTCTCAATGCTGTGTCAGTTTGGTTTCAACTTTAATTTAATATCA 448  
Db 112 LysLeuAsnSerMetIleGlnCysIleSerIleThrValSerIlePheSerLeuValLeu 131  
QY 449 ATTGCAATGTCAGGTATCATATGATAAAACATCCATATCTAATAATTAACACAAAC 508  
Db 132 IleAlaValGluArgHisGlnLeuIleAsnProGlnGlyTyrArgProAsnAsnLys 151  
QY 509 CATGGCTACTTCTGATAGTACTCTGTGGACACTAGGTTTGGCCATCTGTTCTCCCTT 568  
Db 152 HisAlaTyrLeuSerIleValThrMetTyrThrLeuAlaLeuLeuThrSerLeuProPhe 171  
QY 569 CCAGTGTTCACAGTCTTGTGGAACCTTCAAGAAACATTTGGT---TCACATGTCGTGAC 625  
Db 172 LeuLeuPheHisAsnLeuThrAspGluGlnPheHisGlyTyrSerThrGluPheAla 191  
QY 626 AGCAGTATTATGCTGTGAGTCAATGCCATCTGATTCATACAGAAATTCCTTTACTATC 685  
Db 192 GlyLysTyrMetCysLeuGluGlnTyrProSerGluThrGluArgLeuValTyrThr 211  
QY 686 TCTTTATGCTAGTTCAGTATATCTTCCCTTAGTTTGTCTTACTGTAAGTACATCAAGT 745  
Db 212 CysLeuLeuValMetGlnTyrPheAlaProLeuCysPheIlePheIleCysTyrPheLys 231  
RP SEQUENCE FROM N.A.

QY 746 GTCTGCAGAGTATAGCTGTGGATTGTCCACAAAGAACACAGACTTGAAGAAATGAG 805  
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 QY 806 ATGATCAACTTAACTCTTTCATCCATCCAAAGAGTGGGCTCAGGTGAAGAACTCTCTGGC 865  
 Db 232  
 QY 866 AGCCATAATGAGTATTATTCATTCATCAAAACACAGAGAAAGATATAGCAAGACACA 925  
 Db 233  
 QY 926 GCATGTGTGTACCTGCTCCAGAGAGACCTTCTCAAGAGAACCACTCCAGAAATACTTCCA 985  
 Db 244  
 QY 986 GAAACTTTGGCTCTGTGAAGATGAGCTCTTTCATCCAGTAAGTTCATACCAGGGGTC 1045  
 Db 250  
 QY 1046 CCCACTGCTTTGAGATAAACCCTGAAGAAATTCAGATGTTTCATGAATGAGAGTAAAA 1105  
 Db 251  
 QY 1106 CGTCTGTACAGATAAAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTG 1165  
 Db 258  
 QY 1166 ATATTAGTATTGCTGTAGTGGATGACCTACACCTTTTCCATGCTGGTAAGTATT 1225  
 Db 268  
 QY 1226 AATGACAACTTATTCAAAATAGGACATTCAGTGTGTGTGATTCATTTTCTCATTTTGTG 1285  
 Db 288  
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 Db 308  
 QY 1346 GCTCATTTAGTGTCCCTTATACAC 1369  
 Db 328

RESULT 14  
 QY6A5 PRELIMINARY; PRT; 373 AA.  
 ID QY6A5  
 AC QY6A5  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE NPY receptor Y6.  
 OS Squalus acanthias (Spiny dogfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Hyposquala; Squaliformes; Squaloidei;  
 OC Squalidae; Squalus.  
 OX NBI\_TaxID=7797;  
 RN [1]  
 RP MEDLINE=22763539; PubMed=12777532;  
 RX Salaneck E.W., Larson E.T., Larson E.T., Lathammer D.;  
 RA "Three neuropeptide Y receptor genes in the spiny dogfish, Squalus  
 acanthias, support in bloc duplications in early vertebrate  
 evolution."  
 RL Mol. Biol. Evol. 20:1271-1280(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Salaneck E.W., Larson E.T., Larson E.T., Lathammer D.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AY177271; AA062564.1; -

GO: 0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000276; GPCR\_rhodopsn.  
 DR InterPro; IPR000986; Neuroys\_receptor.  
 DR InterPro; IPR000351; NPY1\_receptor.  
 DR InterPro; IPR000611; NPY\_receptor.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PRO0237; GPCRHHODPSN.  
 DR PRINTS; PRO1013; NRPEPTIDEVIR.  
 DR PRINTS; PRO1017; NRPEPTIDEVIR.  
 DR PRINTS; PRO1012; NRPEPTIDEVIR.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 373 AA; 42961 MW; 652E44A1F11DE9F5 CRC64;

Alignment Scores:

Pred. No.: 1.83e-34 Length: 373  
 Score: 522.50 Matches: 117  
 Percent Similarity: 42.44% Conservative: 71  
 Best Local Similarity: 26.41% Mismatches: 134  
 Query Match: 21.07% Indels: 121  
 DB: 7

US-09-771-956-4 (1-1406) x QY6A5 (1-373)

QY 71 TATAACAAGACACTTGCACAGAGAAATAATCTGCTGCCACTCGGAATTTCTGATTTCCCA 130  
 Db 6 TyrAsnHisSerVal-----AsnIleSerGluValIleHisAspGlyThrArgPro 22  
 QY 131 GTCTGGGATGACTATAAAGC-----AGTGTAGATGACTTACAGATATTCTGATGGG 184  
 Db 23 GlnPheAlaAspPheAspSerCysGlnAlaSerProValMetPheLeuLeuLeu 42  
 QY 185 CTCTATACATTTGTAAGTCTTCTGGCTTTATGGGAATCTACTATTATTAATGGCTCTC 244  
 Db 43 AlaTyrGlyThrValThrIleValGlyLeuPheGlyAsnLeuCysLeuIlePheIle 62  
 QY 245 ATGAAAAAGCGTAATACAGAGACTACGGTAACATCTCTCATAGCAATCTGGCTTTCT 304  
 Db 63 LysArgGlnLysGluAsnHisAsnValThrAsnIleLeuIleAlaAsnLeuSerValSer 82  
 QY 305 GATATCTTGTGTGCTGCTTTGCTCACCCTTTCACACTGACGTCTGCTGCTGCTGATCAG 364  
 Db 83 AspValPheIleCysValMetCysIleProPheThrIleValTyrThrLeuMetAspTyr 102  
 QY 365 TGGATGTTTGGCAAGTCATGTCATATTATGCTTTTCTCAATGTGTGTCAGTTTG 424  
 Db 103 TrpIlePheGlyAspIleMetCysLysAlaAsnSerPheIleGlnCysValSerValThr 122  
 QY 425 GTTCAACTTTAATTTAATATCAATTCAGTATCCAGTATCATATCATATAAATCATCCC 484  
 Db 123 ValSerIlePheSerLeuValLeuIleAlaIleGluArgHisGlnLeuIleValAsnPro 142  
 QY 485 ATATCTAATAATTTAAACAGCAACATGGCTACTTCTGATAGTACTGTCTGACACTA 544  
 Db 143 ArgGlyTrpLysProSerValSerHisAlaCysTrpGlyIleValLeuIleTrpPheVal 162  
 QY 545 GGTGTTGCTGCTGTTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACTTCAAGAACA 604  
 Db 163 SerLeuIleIleSerPheProPheIleIlePheHisLeuLeuThrAsp-----GluPro 180  
 QY 605 TTT-----GGTTCAGCATTTGTCAGCAGCAGGAGTATTTATGTTGAGTCA 649  
 Db 181 PheArgAsnValSerSerHisSerGluPheTyrLysAspLysPheValCysIleGluLeu 200  
 QY 650 TGGCATCTGATCATACAGAAATTCCTTACTATCTCTTTATGCTAGTATGCTATATT 709  
 Db 201 TrpProSerGluAlaAspArgLeuValPheThrThrCysLeuLeuIleLeuGlnTyrPhe 220  
 QY 710 CTGCCCCCTAGTTTCTTACTGTAAGTCATACAAGT-----GTCGCAAGAGTATAAGC 763  
 Db 221 AlaProLeuCysPheIlePheValCysTyrLeuLysIlePheValCysLeuLysLysArg 240

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QY 764 TGTGATGTCACAAAGAAAACAGACTTGAGAGAAATGAGATGATCAACTTAACCTTT 823
Db 241 AsnGlyMetAlaAspLys-
QY 824 CATCCATCCAAAAGAGTGGCCCTCAGGTGAACCTCTCTGCGACCCATAATGGAGTTAT 893
Db 246 -----
QY 884 TCATTTCATCAAAAACACAGAAGAAGATATAGCAAGAAGACAGCATGTGTGTACCTGCT 943
Db 246 -----
QY 944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGATACTTCCAGAAAACCTTGGCTCTGTA 1003
Db 247 -----MetArgGluAsnGluSerArgVal-----
QY 1004 AGAAGTCAGCTCTCTTCATCCAGTAAAGTTCATACCAGGGGTCCCACTTGCTTTGAGATA 1063
Db 254 -----
QY 1064 AAACCTGAAGAAAATTCAGATGTCATGAATTGAGAGTAAACGCTTCTGTGTACAGAATA 1123
Db 254 -----
QY 1124 AAAAAGAGATCTCGAAGTGTTTTCTACAGACTGACCATCTGATATTAGTATTGCTGTT 1183
Db 255 ---AsnGluSerLysArgIleAsnMetMetLeuAlaSerIleValAlaPheThrVal---
QY 1184 AGTTGGATGTCACATACCTTTTCCATGTGGTAACTGATTTTAAATGACAATCTTATTTC 1243
Db 274 CysTrpLeuProLeuAsnIlePheAsnValValPheAspTrpAsnHisGluAlaLeuMet 293
QY 1244 AATAGGATTTCAAGTTGGTGTATTGTCATTGTCATTGTTGGTCATGATGCTGTTGT 1303
Db 294 AsnCysHisTrpAsnLeuValPheThrLeuCysHisLeuThrAlaMetIleSerThrCys 313
QY 1304 CTTAATCCAATTCATATGCTGTTTCTTAATAATGGGATTAAAGCTGATTTAGTGTCCCTT 1363
Db 314 IleAsnProIlePheTyrGlyPheLeuAsnLysAsnPheGlnLysAspLeuAsnMetLeu 333
QY 1364 ATACACTGT 1372
Db 334 IleHisCys 336

RESULT 15
AAO62564 PRELIMINARY; PRT; 373 AA.
AC AAO62564;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE NPV receptor Y6.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=22763539; PubMed=12777532;
RA Salanek E., Ardeil D.H., Larson E.T., Larhammar D.;
RT "Three Neuropeptide Y Receptor Genes in the Spiny Dogfish, Squalus
RT acanthias, Support en Bloc Duplications in Early Vertebrate
RT Evolution."
RL Mol. Biol. Evol. 20:1271-1280 (2003).
RN [2]_
RP SEQUENCE FROM N.A.
RA Salanek E.W., Larson E.T., Ardeil D.H., Larhammar D.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY17721; AAO62564.1; -.
KW Receptor.
SQ SEQUENCE 373 AA; 42961 MW; 652E44A1F11DE9F5 CRC64;

Alignment Scores:

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Pred. No.: 1.83e-34 Length: 373
Score: 522.50 Matches: 117
Percent Similarity: 42.44% Conservative: 71
Best Local Similarity: 26.41% Mismatches: 134
Query Match: 21.07% Indels: 121
DB: Gaps: 7

US-09-771-956-4 (1-1406) x AAO62564 (1-373)
QY 71 TATAACAACACACTTCCACAGAGATAATACTGTGCCACTCGGAATTTCTGATTCCCA 130
Db 6 TyrAsnHisSerVal-----AsnIleSerGluValIleHisAspGlyThrArgPro 22
QY 131 GTCCTGGATGACTATAAAGC-----AGTGTAGATGACTTACAGTATTTTCTGATGGG 184
Db 23 GlnPheAlaAspPheAspSerCysGlnAlaSerSerProValMetPheLeuLeuLeuLeu 42
QY 185 CTCATACATTTGTAGTCTTCTGCTTTATGGGGAATCTACTTATTATTAATGCTCTC 244
Db 43 AlaTyrGlyThrValThrIleValGlyLeuPheGlyAsnLeuCysLeuIlePheIleIle 62
QY 245 ATGAAAAGCGTAATCAGAAGACTACGGTAAACTTCTCATAGGCAATCTGCGCTTTTCT 304
Db 63 LysArgGlnLysGluAsnHisAsnValThrAsnIleLeuIleAlaAsnLeuSerValSer 82
QY 305 GATATCTTGGTGTCTGCTTTTCTGCTCACCCTTTCACACTGACGCTCTGCTTCTGATCAG 364
Db 83 AspValPheIleCysValMetCysIleProPheThrIleValTyrThrLeuMetAspTyr 102
QY 365 TGGATGTTGGCAAGTCAATGTGCCATATTATGCTCTTTCTTCAATGTGTGTCAGTTTG 424
Db 103 TrpIlePheGlyAspIleMetCysLysAlaAsnSerPheIleGlnCysValSerValThr 122
QY 425 GTTTCACCTTTAATTTAATATCAATTTGCCATTTGTCAGTATCATATGATAAACAATCCC 484
Db 123 ValSerIlePheSerLeuValLeuIleAlaIleGluArgHisGlnLeuIleValAsnPro 142
QY 485 ATATCTAATAATTTAACGCAACCATGGCTACTTCTTGATAGCTACTGTCTGGACACTA 544
Db 143 ArgGlyTrpLysProSerValSerHisAlaCysTrpGlyIleValLeuIleTrpPheVal 162
QY 545 GGTTTTGCCATCTGTTCTCCCTTCCAGTGTGTTTCACAGTCTTTGTGGAATTCAGAAACA 604
Db 163 SerLeuIleIleSerPheProPheIleIlePheHisLeuLeuThrAsp-----GluPro 180
QY 605 TTT-----GGTTACAGTGTGTCAGCAGCAGTATTTATGTTGTTGAGTCA 649
Db 181 PheArgAsnValSerSerHisSerGluPheTyrLysAspLysPheValCysIleGluIle 200
QY 650 TGGCCATCTGATTTCACAGAAATTCCTTACTATCTTCTTATTTAGTTCAGTATCATTT 709
Db 201 TrpProSerGluAlaAspArgLeuValPheThrThrCysLeuLeuIleLeuGlnTyrPhe 220
QY 710 CTGCCCCTTAGTTGCTTACTTAAGTATACAAAGT-----GTCTGAGAAAGTATAGC 763
Db 221 AlaProLeuCysPheIlePheValCysTyrLeuLysIlePheValCysLeuLysArg 240
QY 764 TGTGATGTCACAAAGAAAACAGACTTGAGAGAAATGAGATGATCAACTTAACCTT 823
Db 241 AsnGlyMetAlaAspLys-----
QY 824 CATCCATCAAAAAGAGTGGGCTCAGGTGAACCTCTCTGCGACCCATAATGGAGTTAT 883
Db 246 -----
QY 884 TCATTTCATCAAAAACACAGAAGAAGATATAGCAAGAAGACAGCATGTGTGTACCTGCT 943
Db 246 -----
QY 944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGATACTTCCAGAAAACCTTGGCTCTGTA 1003
Db 247 -----MetArgGluAsnGluSerArgVal-----

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Qy 1004 AGAAGTCAGCTCTCTTCATCCAGTAAGTTCATACCAGGGTCCCACTTCCTTTGAGATA 1063
Db 254 ----- 254
Qy 1064 AAACCTGAAGAAATTCAGATGTTTCATGAATTGAGAGTAAACGTTCTGTTACAAGAATA 1123
Db 254 ----- 254
Qy 1124 AAAAAGAGATCTCGAAGTGTTCCTACAGACTGACCATCTGATATAGTATTGCTGTT 1183
Db 255 ---AsnGluSerLysArgIleAsnMetMetLeuAlaSerIleValValAlaPheThrVal 273
Qy 1184 AGTTGGATGCCACTACACCTTTCCATGCTGTAAGTATGATGACAAATCTTATTCA 1243
Db 274 CysTrpLeuProLeuAsnIlePheAsnValValPheAspTrpAsnHisGluAlaLeuMet 293
Qy 1244 AATAGGCATTTCAAAGTTGGTGTATTTGTCATTTGTTGGGCATGATGTCCTGTTGT 1303
Db 294 AsnCysHisTyrAsnLeuValPheThrLeuCysHisLeuThrAlaMetIleSerThrCys 313
Qy 1304 CTTAATCCAATCTATATGGGTTTCTTAATAATGGGATTAAGCTGATTTAGTGTCCCTT 1363
Db 314 IleAsnProIlePheTyrGlyPheLeuAsnLysAsnPheGlnLysAspLeuAsnMetLeu 333
Qy 1364 ATACACTGT 1372
Db 334 IleHisCys 336

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Search completed: October 21, 2004, 11:57:50  
Job time : 315.5 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 21, 2004, 11:38:29 ; Search time 42 Seconds  
(without alignments)  
4440.148 Million cell updates/sec

Title: US-09-771-956-4

Perfect score: 2480  
Sequence: 1 tttggtgtgcaaatgt.....attctcactgtttaccagg 1406

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Dgapop 6.0 , Dgapext 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool\_p/US09771956/runat\_21102004\_103738\_9400/app\_query.fasta\_1.1543  
-DB=Issued Patents AA -QMT=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0  
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
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-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
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2: /cgn2\_6/ptodata/1/1aa/5B COMB.pcp:\*  
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4: /cgn2\_6/ptodata/1/1aa/6B COMB.pcp:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description      |
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| 1          | 2386  | 96.2        | 456    | 5     | PCT-US95-15646-4 |
| 2          | 2385  | 96.2        | 455    | 1     | US-08-349-025-4  |
| 3          | 2385  | 96.2        | 455    | 2     | US-08-566-096A-4 |
| 4          | 2385  | 96.2        | 455    | 2     | US-08-668-650B-4 |
| 5          | 2385  | 96.2        | 455    | 3     | US-09-200-673-4  |
| 6          | 2385  | 96.2        | 455    | 4     | US-09-194-895-4  |
| 7          | 2385  | 96.2        | 455    | 4     | US-10-013-846-7  |
| 8          | 2385  | 96.2        | 455    | 4     | US-09-447-907-4  |
| 9          | 2330  | 94.0        | 445    | 2     | US-08-630-118A-6 |
| 10         | 2330  | 94.0        | 445    | 2     | US-08-838-399-6  |
| 11         | 2330  | 94.0        | 445    | 2     | US-09-003-199-21 |
| 12         | 2330  | 94.0        | 445    | 3     | US-09-235-839-6  |

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| 13 | 2330   | 94.0 | 445 | 3 | US-09-327-035-6   | Sequence 6, Appli  |
| 14 | 2330   | 94.0 | 445 | 4 | US-09-065-027-2   | Sequence 2, Appli  |
| 15 | 2330   | 94.0 | 445 | 4 | US-09-708-392-13  | Sequence 13, Appli |
| 16 | 2326   | 93.8 | 445 | 4 | US-09-063-027-4   | Sequence 4, Appli  |
| 17 | 2318   | 93.5 | 445 | 3 | US-09-040-958-2   | Sequence 2, Appli  |
| 18 | 2318   | 93.5 | 445 | 3 | US-09-040-958-4   | Sequence 4, Appli  |
| 19 | 2266   | 91.4 | 445 | 2 | US-09-003-199-2   | Sequence 2, Appli  |
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| 23 | 2084.5 | 84.1 | 456 | 1 | US-08-349-025-2   | Sequence 2, Appli  |
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| 27 | 2084.5 | 84.1 | 456 | 4 | US-09-194-895-2   | Sequence 2, Appli  |
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| 31 | 2074.5 | 83.6 | 445 | 2 | US-08-838-399-4   | Sequence 4, Appli  |
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| 40 | 2067.5 | 83.4 | 445 | 3 | US-09-327-035-2   | Sequence 2, Appli  |
| 41 | 1671   | 67.4 | 334 | 2 | US-08-566-096A-6  | Sequence 6, Appli  |
| 42 | 1671   | 67.4 | 334 | 2 | US-08-668-650B-6  | Sequence 6, Appli  |
| 43 | 1671   | 67.4 | 334 | 3 | US-09-200-673-6   | Sequence 6, Appli  |
| 44 | 1671   | 67.4 | 334 | 4 | US-09-194-895-6   | Sequence 6, Appli  |
| 45 | 1671   | 67.4 | 334 | 4 | US-09-447-907-6   | Sequence 6, Appli  |

## ALIGNMENTS

RESULT 1  
PCT-US95-15646-4  
; General Information:  
; APPLICANT: Syntactic Pharmaceutical Corporation  
; TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR, COMPOUNDS  
; TITLE OF INVENTION: USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC ATYPIC  
; TITLE OF INVENTION: Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF

; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/15646  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 1795/46166-A-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 456 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-15646-4

Alignment Scores:

Pred. No.: 3,786-270 Length: 456  
Score: 2386.00 Matches: 456  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 96.21% Indels: 0  
DB: 5 Gaps: 0

US-09-771-956-4 (1-1406) x PCT-US95-15646-4 (1-456)

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| QY | 17  | ATGCTCTTTTATTCACAGGAGCTATAATATGGATTAGAGCTCGAGAGTATTATTAAC       | 76  |
| Db | 1   | MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn    | 20  |
| QY | 77  | AAGACACTTGCACAGAGATAATATCTGCTGCCACTCGGAATCTCGATTCCAGTCTGG       | 136 |
| Db | 21  | LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr    | 40  |
| QY | 137 | GATGACTATAAAGCAGCTAGATGACTTACAGTATTTCTGATTGGGCTCTATACATTT       | 196 |
| Db | 41  | AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe    | 60  |
| QY | 197 | GTAAGTCTTCTGGCTTTATGGGAATCTACTATTATTTAATGGCTCTCATGAAAAGCGT      | 256 |
| Db | 61  | ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg    | 80  |
| QY | 257 | AATCAGAGACTACGCTAACTCTCTCATAGCAATCTGGCTTTCTCGATATCTTGTT         | 316 |
| Db | 81  | AsnGlnLysThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal       | 100 |
| QY | 317 | GTGCTGTTTGTCTACCTTTTACACAGCTCTGTCTGCTGGATCGATGGATGTTGGC         | 376 |
| Db | 101 | ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuLeuAspGlnTyrMetPheGly | 120 |
| QY | 377 | AAAGTCATGTCATATTATGCTTTCTTCAATGTGTGTCAGTTTGGTTTCACTTTA          | 436 |
| Db | 121 | LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu    | 140 |
| QY | 437 | ATTTTATATCAATGTCAGGTATCATATGATATAAACAATCCATATCTAATAAT           | 496 |
| Db | 141 | IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn    | 160 |
| QY | 497 | TTAACAGAAACCATGGCTACTTCTGTAGTACTGTCTGGACACTAGGTTTGGCATC         | 556 |
| Db | 161 | LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle    | 180 |
| QY | 557 | TGTTCTCCCTTCCAGTCTTTCACAGTCTTGTGGAACCTTCAAGAAACATTTGGTTACGA     | 616 |
| Db | 181 | CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla    | 200 |
| QY | 617 | TGCTGACAGAGATATTATGTTGAGTCATGGCACTGATTATCATACAGAAATGCC          | 676 |
| Db | 201 | LeuLeuSerSerArgTyrLeuCysValGluSerTyrProSerAspSerTyrArgIleAla    | 220 |
| QY | 677 | TTTACTATCTCTTATTTCTAGTTTCAATATCTGCTGCTTCTGCTTCTTCTTCTGTAAGT     | 736 |
| Db | 221 | PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer    | 240 |
| QY | 737 | CATCAAGTGTCTCAGAGATATAAGTGTGGATTGTCCAACAAAGAAACACAGCTTGA        | 796 |
| Db | 241 | HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu    | 260 |
| QY | 797 | GAAATGATGATCACTTAACCTTCTCATCCATCCAAAGAGATGGGCTCAGGTGAAA         | 856 |
| Db | 261 | GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys    | 280 |
| QY | 857 | CTCTCTGACGCCATAATGAGGTATTCTATTCATCAAAAAACACAGAAAGATATAGC        | 916 |
| Db | 281 | LeuSerGlySerHisLysTyrSerTyrSerPheIleLysLysHisArgArgTyrSer       | 300 |

|    |      |   |      |
|----|------|---|------|
| QY | 917  | AAGAAGACAGCATGTGTGTTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA | 976  |
| Db | 301  | LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg  | 320  |
| QY | 977  | ATACTTCCAGAAAACCTTGTGCTCTGTAAAGATGACCTCTCTTCACTCAAGTAACTTCA   | 1036 |
| Db | 321  | IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle     | 340  |
| QY | 1037 | CCAGGGTCCCACTTGTGAGATATAAACCCTGGAAGAAATTCAGATCTTCATGAATG      | 1096 |
| Db | 341  | ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu  | 360  |
| QY | 1097 | AGATATAAAGCTTCTGTTCACAGAAATAAAGAGATCTCGAAGTGTCTTCTACAGACTG    | 1156 |
| Db | 361  | ArgValLysArgSerValThrArgIleLysLysArgSerValPheTyrArgLeu        | 380  |
| QY | 1157 | ACCATACTGATATTAGTATTGCTGTAGTGGATGCCACTACACCTTTTCCATGTGTA      | 1216 |
| Db | 381  | ThrIleLeuIleLeuValPheAlaValSerTyrMetProLeuHisLeuPheHisValVal  | 400  |
| QY | 1217 | ACTGATTTTAAATGACAACTCTTATTTCAAATAGGCATTTCAAGTTGGTGTATTGCTTGT  | 1276 |
| Db | 401  | ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys  | 420  |
| QY | 1277 | CATTGTTGGCATGATGCTGTTGCTTAATCCAAATCTATATGGGTTTCTTAAATAT       | 1336 |
| Db | 421  | HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn  | 440  |
| QY | 1337 | GGGATTAAGAGCTGATTAGTGTCCCTTATACACTGTCTTCATATGTA               | 1384 |
| Db | 441  | GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet**               | 456  |

RESULT 2

US-08-349-025-4  
Sequence 4, Application US/08349025  
Patent No. 5602024  
GENERAL INFORMATION:  
APPLICANT: Gerald, Christophe P.G.  
APPLICANT: Walker, Mary W.  
APPLICANT: Branchek, Theresa  
APPLICANT: Weinshank, Richard L.  
TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL  
NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/349,025  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1795/46166  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-349-025-4

Alignment Scores:  
Pred. No.: 4,94e-270 Length: 455  
Score: 2385.00 Matches: 455  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 96.17% Indels: 0  
DB: 1 Gaps: 0

US-09-771-956-4 (1-1406) x US-08-349-025-4 (1-455)

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| DB | 1   | MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn | 20  |
| QY | 77  | AAGACATGTCACAGAGATAAATCTGCTCCCACTCGGAATCTGATTTCCAGCTGG       | 136 |
| DB | 21  | LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr | 40  |
| QY | 137 | GATGACTATAAAGCAGTGTAGACTTACAGTATTCTTCTGATTGGCTCTATACATTT     | 196 |
| DB | 41  | AspAspTyrLysSerSerValAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe    | 60  |
| QY | 197 | GTAAGTCTCTTGGCTTTATCGGAATCTACTTATTTAATGCTCTCATGAAAACGCT      | 256 |
| DB | 61  | ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg | 80  |
| QY | 257 | AATCGAAGACTACGTTAACTTCTCATAGCAATCTGGCTTTCTGATATCTTGGTT       | 316 |
| DB | 81  | AsnGlnLysThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspLeuVal       | 100 |
| QY | 317 | GTGCTGTTTGTCTACCTTTTACACTGACGCTCTGTTCTGTCGATCATGAGTATTGGC    | 376 |
| DB | 101 | ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTyrMetPheGly | 120 |
| QY | 377 | AAAGTCATGTCGCATATATGCTTTCTTCAATGTGTCTCAGTTTGGTTTCAACTTA      | 436 |
| DB | 121 | LysValMetCysHisLeuMetProPheLeuGlnCysValSerValLeuValSerThrLeu | 140 |
| QY | 437 | ATTTTAAATCAATGGCAATGTCAAGTATCATATGATAAAACATCCCATATCTAAAT     | 496 |
| DB | 141 | IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn | 160 |
| QY | 497 | TTACAGCAAAACCATGGTACTTTCTGATAGTACTGTCTGACACTAGTTTGGCATC      | 556 |
| DB | 161 | LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle | 180 |
| QY | 557 | TGTTCTCCCTTCCAGTCTTTCACAGTCTTGTGGAACTTCAAGAACATTTGGTTACGA    | 616 |
| DB | 181 | CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla | 200 |
| QY | 617 | TTGCTGAGCAGCAGGTATTATGTTGTGATGTCATGCCATCTGATTCATACAGAAATGCC  | 676 |
| DB | 201 | LeuLeuSerSerArgTyrLeuCysValGluSerTyrProSerAspSerTyrArgIleAla | 220 |
| QY | 677 | TTTACTATCTTTATGCTAGTTCAGTATATCTGCTTGTAGTTTCTTACTCTAGT        | 736 |
| DB | 221 | PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer    | 240 |
| QY | 737 | CATACAGTGTCTGCAGAAAGTATAAGCTGTGATTGTCCAAACAAAGAAAACAGACTTGA  | 796 |
| DB | 241 | HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu | 260 |
| QY | 797 | GAATATGATGATCACTAACTTCTTTCATCCATCAAAAGAGTGGGCTCAGGTGAAA      | 856 |
| DB | 261 | GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys | 280 |
| QY | 857 | CTCTCTGGCAGCATTAATGGAGTATTCTCATCAAAACACAGAGAGATATAGC         | 916 |
| DB | 281 | LeuSerGlySerHisLysTyrSerPheIleLysLysHisArgArgArgTyrSer       | 300 |

|    |      |   |      |
|----|------|---|------|
| QY | 917  | AAGAAGACAGCATGTGTGTATTACCTCTCCAGAAAACCTTCTCAAGAGAACCTCCAGA    | 976  |
| DB | 301  | LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg  | 320  |
| QY | 977  | ATACTTCCAGAAAACCTTTGGCTCTCTAAGAAGTCTGCTCTTTCATCCAGTAAAGTTTATA | 1036 |
| DB | 321  | IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle     | 340  |
| QY | 1037 | CCAGGGGTCCCACTTGTCTTTCAGATAAAACCTGAAGAAAATTCAGATGTTTCATGAATG  | 1096 |
| DB | 341  | ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu  | 360  |
| QY | 1097 | AGAGTAAACCTTCTTACAGAAATAAAGAGATCTCGAAGTGTCTTCTACAGACTG        | 1156 |
| DB | 361  | ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheLysArgLeu  | 380  |
| QY | 1157 | ACCATACTCATATTACTTATTTCTGTTAGTTCGATGCCACTACACCTTTTCCATGTGTA   | 1216 |
| DB | 381  | ThrIleLeuIleLeuValPheAlaValSerTyrMetProLeuHisLeuPheHisValVal  | 400  |
| QY | 1217 | ACTGATTTTAAATGACAACTTATTTTCAATAGAGCATTCACAGTTGGTGTATTCATTTCT  | 1276 |
| DB | 401  | ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys  | 420  |
| QY | 1277 | CATTTCTTGGCATGATGCTCTGTTCTTAAATCCAATCTATATGGGTTCCTTAATAAT     | 1336 |
| DB | 421  | HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn  | 440  |
| QY | 1337 | GGGATTTAAAGCTGATTTAGTGTCCCTTATACACTGTCTTTCATATG               | 1381 |
| DB | 441  | GlyLeuLysAlaAspLeuValSerLeuIleHisCysLeuHisMet                 | 455  |

RESULT 3

US-08-566-096A-4  
; Sequence 4, Application US/08566096A  
; Patent No. 5968819  
; GENERAL INFORMATION:  
; APPLICANT: Getald, Christophe P.G.  
; APPLICANT: Walker, Mary W.  
; APPLICANT: Branchek, Theresa  
; APPLICANT: Weinschank, Richard L.  
; TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR, DNA ENCODING A HYPOTHALAMIC  
; TITLE OF INVENTION: COMPOUNDS USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC  
; TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/566,096A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 1795/46166-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid



TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-668-650B-4

Alignment Scores:  
Pred. No.: 4,94e-270 Length: 455  
Score: 2385.00 Matches: 455  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 96.17% Indels: 0  
DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x US-08-668-650B-4 (1-455)

|    |     |   |     |
|----|-----|---|-----|
| Qy | 17  | ATGCTCTTTTATCCAGCAGGACTATAATATGAGTTAGAGCTCGACGAGTATTATAC        | 76  |
| Db | 1   | MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrAsn       | 20  |
| Qy | 77  | AAGACATTCGCACAGAGATAATACCTGCTGCCACTCGGAATCTGATTTCCCGAGCTGG      | 136 |
| Db | 21  | LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTip    | 40  |
| Qy | 137 | GATCAGTATAAAGCAGTAGATGACTTACAGTATTTCTGATTTGGGCTCTATACATTT       | 196 |
| Db | 41  | AspAspTyrLysSerSerValAspLeuGlnTyrPheLeuLeuGlyLeuTyrThrPhe       | 60  |
| Qy | 197 | GTAAGTCTTCTGCTTATGGGAATCTACTTATTTAATGGCTCTCATGAAAGCGT           | 256 |
| Db | 61  | ValSerLeuLeuGlyPheMetGlyAsnLeuLeuLeuMetAlaLeuMetLysLysArg       | 80  |
| Qy | 257 | AATCAGAGACTACGGTAAACTTCTCTCATAGCAATCTGGCCTTTTCTGATATCTGGTT      | 316 |
| Db | 81  | AsnGlnLysThrThrValAsnPheLeuLeuLeuGlyAsnLeuAlaPheSerAspIleLeuVal | 100 |
| Qy | 317 | GTGCTGTTTCTCACCTTTCACACTGACGCTCTGCTGCTGGATCAGTGGATTTGGC         | 376 |
| Db | 101 | ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly    | 120 |
| Qy | 377 | AAAGTCATGTCCTATATATCTCTTCTCAATGTGTGTCAGTGTGGTTTCAACATTA         | 436 |
| Db | 121 | LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu    | 140 |
| Qy | 437 | ATTTTATATCAATGGCAATGTCAGGTATCATATGATAAACAATCCATCTCAATAAT        | 496 |
| Db | 141 | IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn    | 160 |
| Qy | 497 | TTACAGCAAAACCATGGCTACTTTCTGATAGCTACTGTCGACACTAGGTTTGGCCATC      | 556 |
| Db | 161 | LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle    | 180 |
| Qy | 557 | TGTTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACCTCAAGAAACATTTGGTTCAGCA      | 616 |
| Db | 181 | CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla    | 200 |
| Qy | 617 | TTGCTGACAGCAGTATTTATGTTGTGAGTCAGTCGCCATCTGATTCATACAGAAATGCC     | 676 |
| Db | 201 | LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla    | 220 |
| Qy | 677 | TTTACTATCTTTTATGCTAGTTCAGTATATTTCTGCCCTTAGTTTGTCTTACTGTAAGT     | 736 |
| Db | 221 | PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer    | 240 |
| Qy | 737 | CATCAAGTGTCTGAGAGTATAGCTGTGGATTTGTCCAAAGAAAGAAACAGACTTGAA       | 796 |
| Db | 241 | HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu    | 260 |
| Qy | 797 | GAAATGAGATGATCACTTACTCTTCATCCATCCAAAGAGTGGCCCTCAGGTGAAA         | 856 |
| Db | 261 | GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys    | 280 |
| Qy | 857 | CTCTCTGGCAGCCATAAATGGAGTATTCAATTCATCAAAAACACAGAGAGATATAGC       | 916 |

|    |      |  |      |
|----|------|--|------|
| Db | 281  | LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer      | 300  |
| Qy | 917  | RAGRAGACAGCATGTGTATTACCTGCTCCAGAAAGACCTTCTCAAGAGAACACCTCCAGA   | 976  |
| Db | 301  | LysLysThrAlaCysValLeuProIleProGluArgProSerGlnGluAsnHisSerArg   | 320  |
| Qy | 977  | ATPACTTCCAGAAACTTTGGCTCTGTAAAGAGTCAGCTCTCTTTCATCCAGTAAAGTTTATA | 1036 |
| Db | 321  | IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle      | 340  |
| Qy | 1037 | CCAGGGTCCCACTGCTTTGAGATAAAGCTGAGAAATTCAGATGTTTCATCAATTTG       | 1096 |
| Db | 341  | ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu   | 360  |
| Qy | 1097 | AGAGTAAAAACGTTCTGTTTACAGAAATAAAAGAGATCTCGAAGTGTTCCTTACAGATG    | 1156 |
| Db | 361  | ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu   | 380  |
| Qy | 1157 | ACATACACTGATATTAGTATTCTGCTGTTAGTGGATGCCACTACACCTTTCCATCTGGTA   | 1216 |
| Db | 381  | ThrIleLeuIleValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal      | 400  |
| Qy | 1217 | ACTGATTTTAAATGACAACTTATTTCAATAGGCATTTCAAGTTGGTGTATTGCAATTTGT   | 1276 |
| Db | 401  | ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys   | 420  |
| Qy | 1277 | CATTTGTTGGGCAATGATGTCCTGTTGCTTAAATCCAAATCTATATGCGTTCCTTAATAT   | 1336 |
| Db | 421  | HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn   | 440  |
| Qy | 1337 | GGATTAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG                    | 1381 |
| Db | 441  | GlyIleLysAlaAspLeuValSerIleIleHisCysLeuHisMet                  | 455  |

RESULT 5

US-09-200-673-4  
; Sequence 4, Application US/09200673A  
; Patent No. 6316203  
; GENERAL INFORMATION:  
; APPLICANT: Gerald, Christophe P.G.  
; APPLICANT: Weinshank, Richard L.  
; APPLICANT: Walker, Mary W.  
; APPLICANT: Branchek, Theresa  
; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful  
; TITLE OF INVENTION: in Such Methods and DNA Encoding A Hypothalamic  
; TITLE OF INVENTION: Acyclical Neuropeptide Y/Peptide YY Receptor (Y5)  
; FILE REFERENCE: 46166-BZ/JPW  
; CURRENT APPLICATION NUMBER: US/09/200,673A  
; EARLIER FILING DATE: 1998-11-25  
; EARLIER APPLICATION NUMBER: 09/566,096  
; EARLIER FILING DATE: 1995-12-01  
; EARLIER APPLICATION NUMBER: 08/349,025  
; EARLIER FILING DATE: 1994-12-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-200-673-4

Alignment Scores:  
Pred. No.: 4,94e-270 Length: 455  
Score: 2385.00 Matches: 455  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 96.17% Indels: 0  
DB: 3 Gaps: 0

US-09-771-956-4 (1-1406) x US-09-200-673-4 (1-455)

|    |    |  |    |
|----|----|--|----|
| Qy | 17 | ATGCTCTTTTATCCAGCAGGACTATAATATGAGTTAGAGCTCGACGAGTATTATAC | 76 |
|----|----|--|----|

Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20  
 QY 77 AGACACATGCGCACAGAGATAATCTGCTGCCACTCGGAATTCGATTCCCGAGTCGG 136  
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40  
 QY 137 GATGACTATAAAGCAGCTAGATCAGTACAGTATTTCTGATGGGCTCTATACATTT 196  
 Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60  
 QY 197 GTAAGTCCTCTTGGCTTTATGGGGAATCTACTATTATTTAATGGCTCTCATGAAAAGCGT 256  
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80  
 QY 257 AATCAGAGACTACGGTAAACTTCTCATAGCAATCTGGCTTTTCTGATATCTTGGTT 316  
 Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100  
 QY 317 GFGCTGTTTGGCTACCTTTACACTGACAGCTGTCTGCTGGATCGAGTCTTGGC 376  
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTyrMetPheGly 120  
 QY 377 AAAGTCATGTCGCATATATGCTTTCTCTCAATGTGTGTCAGTTTGGTTTCACTTA 436  
 Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140  
 QY 437 ATTTTAAATATCAATGTCATGTCAGGTATCATATGATATAAACATCCATATCTAATAAT 496  
 Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160  
 QY 497 TTAACAGAAACCATGCTGCTACTTCTGATAGTCTGTCGACACTAGGTTTGGCATC 556  
 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle 180  
 QY 557 TGTTCTCCCTTCCAGTCTTTCACAGTCTTGTGAACCTTCAAGAAACATTTGGTTTCAGCA 616  
 Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200  
 QY 617 TTGCTGACGACAGATATTTATGTGTGAGTCATGGCACTGATCTCATACAGAAATGCC 676  
 Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTyrProSerAspSerTyrArgIleAla 220  
 QY 677 TTTACTATCTCTTTATCTAGTTTCAGTATATCTGCTTCTGCTTCTGCTTCTGTAAGT 736  
 Db 221 PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240  
 QY 737 CATACAAGTGTCTCAGAAATATAGCTGTGGATGTCCAAACAAAGAAACACAGCTTGAA 796  
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260  
 QY 797 GAAATGAGATGATCAACTTAACCTTCACTCCATCCAAAGAGTGGGCTCAGGTGAAA 856  
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280  
 QY 857 CTCTCTGCGACCCATAATGAGTATTAATTCATTCATCAAAACACAGAAAGATATAGC 916  
 Db 281 LeuSerGlySerHisLysTyrSerTyrSerPheIleLysLysHisArgArgGlySer 300  
 QY 917 AAGAAGACAGATGTGTGTTACCTGCTCCAGAAAGACTTCTCAAGAGAACCCATCCAGA 976  
 Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320  
 QY 977 ATACTTCCAGAAAATCTTGGCTCTGTGAAGAGTCAAGTCTCTTCTCATCCAGTAAGTTTCA 1036  
 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340  
 QY 1037 CCAGGGTCCCCTTCTGTTTGAATATAAACCTGAGAAAATTCAGATGTTTCATGAATTG 1096  
 Db 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360  
 QY 1097 AGAGTAAACCTTCTGTTTACAGAAATAAAGAGATCTCGAAGTGTTTCTTCTACAGACTG 1156  
 Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380

QY 1157 ACCATACTGATATTAGTATTTCGCTGTAGTTCGACCTACACCTTTTCCATGTGTA 1216  
 Db 381 ThrIleLeuIleLeuValPheAlaValSerTyrMetProLeuHisLeuPheHisValVal 400  
 QY 1217 ACTGATTTTAAATGACAAATCTTATTTCAAATAGGCATTTCAAGTTGTGTGTTGCAATTTGT 1276  
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420  
 QY 1277 CATTTGTTGGCATGATGCTGCTGTCTTCTTAATCCAAATCTATATGGGTTTCTTAATAAT 1336  
 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
 QY 1337 GGGATTAAGAGCTGATTAGTGTCCCTTATACACTGTCTTCATATG 1381  
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455  
 RESULT 6  
 US-09-194-895-4  
 ; Sequence 4, Application US/09194895  
 ; Patent No. 6531287  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerald, Christophe P.G.  
 ; APPLICANT: Weinshank, Richard L.  
 ; APPLICANT: Walker, Mary M  
 ; APPLICANT: Branche, Theresa  
 ; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful  
 ; TITLE OF INVENTION: In Such Methods, and DNA Encoding A Hypochalamic  
 ; TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (Y5)  
 ; FILE REFERENCE: 1795-46166-D-PCT-US/JPW/BJA  
 ; CURRENT APPLICATION NUMBER: US/09/194,895  
 ; PRIOR FILING DATE: 1999-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US97/09504  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 455  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-194-895-4  
 Alignment Scores:  
 Pred. No.: 4,94e-270 Length: 455  
 Score: 2385.00 Matches: 455  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 96.17% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-956-4 (1-1406) x US-09-194-895-4 (1-455)  
 QY 17 ATGCTTTTATCCAGCAGACTATATATGATGATTTAGAGCTCGACAGTATTATAAC 76  
 Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20  
 QY 77 AGACACATGCGCACAGAGATAATCTGCTGCCACTCGGAATTCGATTCCCGAGTCGG 136  
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40  
 QY 137 GATGACTATAAAGCAGCTAGATCAGTACAGTATTTTCTGATGGGCTCTATACATTT 196  
 Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60  
 QY 197 GTAAGTCCTCTTGGCTTTATGGGGAATCTACTATTATTTAATGGCTCTCATGAAAAGCGT 256  
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80  
 QY 257 AATCAGAGACTACGGTAAACTTCTCATAGCAATCTGGCTTTTCTGATATCTTGGTT 316  
 Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100  
 QY 317 GFGCTGTTTGGCTACCTTTACACTGACGCTCTGCTGCGATCAGTGGATGTTTGGC 376

101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120  
377 AAAGTCATGCGCATATATATGCGCTTTCTTCAATGTGTGTGTCAGTGTGGTTTCAACTTTA 436  
121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140  
437 ATTTTATATCAATTGCGCATGTCAGTATCATATGATATAAAACATCCCATATCTATAAT 496  
141 IleLeuLeuSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsn 160  
497 TTAACAGCAAAACCATGCTACTTCTCATAGCTACTCTGCGACACTAGGTTTGGCATC 556  
161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180  
557 TGTTCTCCCTCCAGTGTGTTTACAGTCTTGTGGAACCTCAAGAACATTTGGTTGACGA 616  
181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnThrPheGlySerAla 200  
617 TTGCTGAGCAGCAGTATTTATGTTGAGTCTGAGTCCATCTCATACACAATGTC 676  
201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220  
677 TTTACTATCTCTTATGCTAGTTCAGTATATTTCTGCCCTTAGTTGTCTTACTGAAGT 736  
221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240  
737 CATCAAGTCTCCAGAGATATAGCTGTGGATTGTCACCAAGAAAGAACACACTGAA 796  
241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260  
797 GAAATCAGATGATCAACTTAACTCTTCAATCCATCCAAAAGAGTGGCGCTCAGGTGAA 856  
261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280  
857 CTCTCTGGCGCCATAAATGGAGTTTATTCATTCATAAAAAACACAGAAAGATATAGC 916  
281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300  
917 AAGAAGCAGCATGTGTGTACCTGCTCCAGAAAGACCTTCTCAAGAAACCACTCCAGA 976  
301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320  
977 ATACTTCCAGAAAACCTTGGCTGTGTAAGAGTCAGTCTCTTCATCCAGTAAGTTGATA 1036  
321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340  
1037 CCAGGGTCCCACTGCTTGTGATATAAACCTCAAGAAATTCAGATGTTTCATGATTG 1096  
341 ProGlyValProThrCysPheGluIleLysProGluAsnSerAspValHisGluLeu 360  
1097 AGAGTAAACCTTCTGTACAGAAATAAAAGAGATCTCGAAGTGTGTTTCTACAGACTG 1156  
361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380  
1157 ACCATCTGATATATGATTTGCTGTGTAGTTGGATGCCACTACACCTTTCCATGGGTA 1216  
381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400  
1217 ACTGATTTAATGACAATCTTATTTCAATAGGCAATTCAGTTGGTGTATGTCATTGT 1276  
401 ThrAspPheAsnAspAsnLeuLysSerAsnArgHisPheLysLeuValTyrCysIleCys 420  
1277 CATTTGTTGGCAGTATGCTGTGTCTTAAATCCAAATCTATATGGGTTTCTTAATAT 1336  
421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
1337 GGGATTAAGCTGATTTAGTCTCCCTTATACACATGCTCTTCATATG 1381  
441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 7  
US-10-013-846-7

; Sequence 7, Application US/10013846  
; Patent No. 6S86367  
; GENERAL INFORMATION:  
; APPLICANT: Bakthavatchalam, Rajagopal  
; APPLICANT: Blum, Charles A  
; APPLICANT: Brielmann, Harry L  
; APPLICANT: Darrow, James W  
; APPLICANT: De Lombaert, Stephane  
; APPLICANT: Hutchison, Alan  
; APPLICANT: Tran, Jennifer  
; APPLICANT: Zheng, Xiaozhang  
; APPLICANT: Elliott, Richard L  
; APPLICANT: Hammond, Marlys  
; TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and  
; 3H-spiroisobenzofuran-1,4'-piperidines  
; FILE REFERENCE: N00.2001  
; CURRENT APPLICATION NUMBER: US/10/013,846  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 60/254,990  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: homosapiens  
; US-10-013-846-7

Alignment Scores:  
Pred. No.: 4,948-270 Length: 455  
Score: 2385.00 Matches: 455  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 96.17% Indels: 0  
Gaps: 0  
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US-09-771-956-4 (1-1406) x US-10-013-846-7 (1-455)

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QY 77 AAGACACTTGCACAGAGATTAATACTGCTGCGCACTCGGAATTCGATTTCCAGTCTGG 136  
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QY 137 GATGACTATAAAAGCAGCTAGATCACTTACAGTATTTTCTGATTTGGGCTCTTACATTT 196  
Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60  
QY 197 GTAAGTCTTCTGCTTTATGGGGAATCTACTATTTTAAATGCTCTCATGAAAAGCGT 256  
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80  
QY 257 AATCAAGACACTACGTAACCTTCCTCATAGGCAATCTGGCCTTTTCTGATATCTTGGTT 316  
Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100  
QY 317 GTGCTGTTTGTCACTTTCACATGAGTCTGCTTGTCTGGATCAGTGGATGTTTGGC 376  
Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120  
QY 377 AAGTCACTGCGCATATATGCTTTTCTCAATGTGTCTAGTTTGTGTTTCAACTTTA 436  
Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140  
QY 437 ATTTTAAATATCAATTTGCCATTTGCGAGTATCATATGATATAAAACATCCCATATCTAATA 496  
Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsn 160  
QY 497 TTAACAGCAAAACCATGCTACTTCTCATAGCTACTCTGCGACACTAGGTTTGGCATC 556  
Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180

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557 TGTCTCCCTCCAGTCTTTACAGTCTTGTGGAACCTTCAAGAAACATTTGGTTCAGCA 616
181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnThrPheGlySerAla 200
617 TTGCTGACAGCAGATATTATGCTTGCAGTCATGCGCCATCTGATTCATACAGAAATGCC 676
201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
677 TTTACTATCTCTTATCTAGTTCAGTATATCTGCGCTTGTAGTTTGTCTTACTGTAAGT 736
221 PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
737 CATACAGTGTCTGAGAAATATAGCTGTGATGTTCCAAAGAAACACAGACTTGA 796
241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
797 GAATATGATGATCACTTAACTTCTCATCTTCAATCCAAAGAGTGGCGCTCAGGTGAA 856
261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
857 CTCTCTGCGCAGCCATTAATGAGTATTATTCATTCATCAAAAAACACAGAAAGATAGC 916
281 LeuSerGlySerHisLysTyrSerTyrSerPheIleLysLysHisArgTyrSer 300
917 AGAAGACAGCATGTGTTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA 976
301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
977 ATACTTCCAGAAAACCTTTGGCTCTGTAAAGAGTCAGCTCTCTTCATCCAGTAAGTTCATA 1036
321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
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361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
1157 ACCATPACTGATATTAGTATTGCTGTAGTTGATGATGATGATGATGATGATGATGATGAT 1216
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401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
1277 CATTTGTTGGGCATGATCTCTGTTGTTTATCAATCAATTCATATGCGTGTCTTATAAT 1336
421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
1337 GGGATTAAGCTGATTAGTGTCCCTTATACACTGCTCTCTATATG 1381
441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

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RESULT 8

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US-09-447-907-4
; Sequence 4, Application US/09447907
; Patent No. 6645774
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Weinschank, Richard L.
; APPLICANT: Walker, Mary W.
; APPLICANT: Branchek, Theresa
; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful in Such M
; FILE REFERENCE: 1795-46166CA
; CURRENT APPLICATION NUMBER: US/09/447,907
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 08/668,650
; PRIOR FILING DATE: 1996-06-04

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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Y5 cDNA clone
US-09-447-907-4

Alignment Scores:
Pred. No.: 4 94e-270 Length: 455
Score: 2385.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.17% Indels: 0
DB: Gaps: 0

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QY 17 ATGCTCTTTTATTCGAAGCAGACTATATATGATTTAGAGCTCGACAGTATTATTAAC 76
Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
QY 77 AAGACACTTGCACAGAGATAATACTGCTGCCTCGAAATTCCTGATTTCCAGTCTGG 136
Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40
QY 137 GATGACTATAAAGCAGGTGTAGATCACTTACAGTATTTTCTGATTGGCTCTATACATT 196
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QY 197 GTAACTCTCTTGGCTTATGGGAATCTACTATTTTAAATGGCTCTCATGAAAAGCGT 256
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QY 257 AATCAGAACACTACGTAACCTTCCTCATAGGCAATCTGGCTTTTCTGATATCTTGTT 316
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QY 377 AAAGTCATGTGCAATATTATGCTTTTCTCAATGTGTCTGCTGAGTCTTTCGTTTCAACTTTA 436
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Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
QY 497 TTAACAGCAAAACATGGCTACTTCTGATAGTACTGTCTGACACTAGGTTTTCGCCATC 556
Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
QY 557 TGTCTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACTTTCAGAAACATTTGGTTCAGCA 616
Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGlnThrPheGlySerAla 200
QY 617 TTGCTGACAGCAGGATTTATGCTTGCAGTCATGCGCCATCTGATTCATACAGAAATGCC 676
Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
QY 677 TTTACTATCTCTTATCTAGTTCAGTATATCTGCGCTTGTAGTTTGTCTTACTGTAAGT 736
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QY 737 CATACAGTGTCTGAGAAATATAGCTGTGATGTTCCAAAGAAACACAGACTTGA 796
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261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280  
 857 CTCTCTGGCCACCAATAAGTATTCATTCATCAAAACACACAGAAAGATATAGC 916  
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 917 AAGAAGACAGCATGTGTGTACCTGCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA 976  
 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320  
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 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340  
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 341 ProGlyValProThrCysPheGluIleLysProGluAsnSerAspValHisGluLeu 360  
 1097 AGACTAAACGCTTCTGTACAGAAATAAAGAGATCTCGAAGTGTCTTCTCAGACTG 1156  
 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380  
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 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420  
 1277 CATTTGTTGGCAGTATGCTCTGTGTCTTAACTCAATTCATATGGTGTCTTAAATAAT 1336  
 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
 1337 GGGATTAAGCTGATTAGTCTCCCTTATACATACATGCTCTTCATATG 1381  
 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 9

US-08-630-118A-6  
 ; Sequence 6, Application US/08630118A  
 ; Patent No. 5919901  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hu Ph.D., Yinghe  
 ; APPLICANT: McCaleb Ph.D., Michael L.  
 ; APPLICANT: Bloomquist Ph.D., Brian T.  
 ; APPLICANT: Flores-Riveros Ph.D., Jaime R.  
 ; APPLICANT: Cornfield Ph.D., Linda J.  
 ; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
 ; TITLE OF INVENTION: Sequences  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
 ; STREET: 300 South Wacker Drive, 32nd Floor  
 ; CITY: Chicago  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/630,118A  
 ; FILING DATE: April 8, 1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Greenfield Ph.D., Michael S.  
 ; REGISTRATION NUMBER: 37,142  
 ; REFERENCE/DOCKET NUMBER: 96,149/WH 405  
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)715-1000  
 TELEFAX: (312)715-1234  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 445 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-630-118A-6  
 Alignment Scores:  
 Pred. No.: 1,34e-263 Length: 445  
 Score: 2330.00 Matches: 445  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.95% Indels: 0  
 DB: 2 Gaps: 0  
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 QY 107 GCACCTCGGAATTCTGATTTCCTCCAGTCTGGGATGACTATATAAAGCAGGTAGATGACTTA 166  
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40  
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 QY 467 CATATCAATAAACATCCCATATCTAATAATTTAAACAGCAACCATGGCTACTTCTGATA 526  
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;
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-399-6

Alignment Scores:
Pred. No.: 1,34e-263 Length: 445
Score: 2330.00 Matches: 445
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.95% Indels: 0
DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x US-08-838-399-6 (1-445)

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QY 167 CAGTATTTCTGATGGGCTCTATACANTTGTAACTCTCTTGGCTTTATGGGAATCTA 226
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QY 287 GGCATCTGGCCTTTCTGATATCTTGGTGTGCTGTTTGTCTCACCCTTCACACTGAGC 346
Db 81 GlyAsnLeuAlaPheSerAspLeuValLeuValPheCysSerProPheThrLeuThr 100
QY 347 TCTGTCTCTGCTGATCAGTGGAGTGTTCGCAAGTCATGTGCCATATTATGCTTTCTT 406
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisLleMerProPheLeu 120
QY 407 CAATGTGTGCTAGTTTGGTTTCAACTTAATTTAATATCAATGCCATGTCAGGTAT 466
Db 121 GlnCysValSerValLeuValSerThrLeuLeuLeuLeuSerLeuAlaValArgTyr 140
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QY 767 GGATTGTCCAAACAAAGAAACAGACTTCGAAGAAATGAGATGATCAACTTAACCTTTCAT 826
Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetLleAsnLeuThrLeuHis 260
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RESULT 10

US-08-838-399-6  
; Sequence 6, Application US/08838399  
; Patent No. 5965392

GENERAL INFORMATION:

APPLICANT: Hu Ph.D., Yinghe  
APPLICANT: McCaleb Ph.D., Michael L.  
APPLICANT: Bloomquist Ph.D., Brian T.  
APPLICANT: Flores-Riveros Ph.D., Jaime R.  
APPLICANT: Cornfield Ph.D., Linda J.  
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

TITLE OF INVENTION: Sequences

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boenhen Fulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,399  
FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Greenfield Ph.D., Michael S.  
REGISTRATION NUMBER: 37,147  
REFERENCE/DOCKET NUMBER: 96,149/WH 405  
TELECOMMUNICATION INFORMATION:

Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280  
Qy 887 TTTATCAAAAACACAGAGAAGATATAGCAAGACAGACATGTGTCTACCTGCTCCA 946  
Db 281 PheileLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
Qy 947 GAAAGACCTTCTCAAGAGAACCTCCAGATACTCCAGAAACTTTGGCTCTGTAAGA 1006  
Db 301 GluArgProSerGlnGluAsnHisSerArgLleuProGluAnPheGlySerValArg 320  
Qy 1007 AGTCAGCTCTCTTCATCCAGTAAGTTTCATACCCAGGGTCCCCACTTCCTTTGAGATAAAA 1066  
Db 321 SerGlnLeuSerSerSerLysPheileProGlyValProThrCysPheGluileLys 340  
Qy 1067 CCTGAAGAAANTTCAGATGTTTCAGATTGAGATAAAGCTTCTGTATCAAGATAAAA 1126  
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Db 441 HisCysLeuHisMet 445

RESULT 11  
US-09-003-199-21  
; Sequence 21, Application US/09003199  
; Patent No. 5985616  
; GENERAL INFORMATION:  
; APPLICANT: Parker, Eric M  
; APPLICANT: Strader, Catherine D  
; APPLICANT: Rudinski, Mark S  
; TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schering-Plough Corporation  
; STREET: 2000 Galloping Hill Road  
; CITY: Kenilworth  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07033-0530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.5.3  
; SOFTWARE: Microsoft Word 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,199  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thampoe, Immac J.  
; REGISTRATION NUMBER: 36,322  
; REFERENCE/DOCKET NUMBER: CN0775  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)298-5061  
; TELEFAX: (908)298-5388  
; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-003-199-21  
Alignment Scores:  
Pred. No.: 1,34e-263 Length: 445  
Score: 2330.00 Matches: 445  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.95% Indels: 0  
DB: 2 Gaps: 0  
US-09-771-956-4 (1-1406) x US-09-003-199-21 (1-445)  
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Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20  
Qy 107 GCCACTCGGAATTTCTGATTTCCAGTCTGGGATGACTATAAAAGCAGTGTAGTACACTTA 166  
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Qy 167 CAGTATTTTCTGATTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTA 226  
Db 41 GlnTyrPheLeuileGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
Qy 227 CTTATTTTAAATGGCTCTCATGAAAAGCGTAATCAGAAGACTACGTAACCTTCCTCAT 286  
Db 61 LeuileLeuMetAlaLeuMetLysArgAsnGlnLysThrValAsnPheLeuile 80  
Qy 287 GGCAATCTGGCCCTTTTCTGATATCTTGGTGTGCTGCTTTTGTCTACCTTTACACTGAGC 346  
Db 81 GlyAsnLeuAlaPheSerAspLeuValLeuValPheCysSerProPheThrLeuThr 100  
Qy 347 TCTGCTTCTGATCAGTGGATGTTTGGCAAGTCAATGTCATATATGCTTTCTT 406  
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120  
Qy 407 CAATGTGTCTCAGTGTGTTTGGTTTCACTTTAAATTTTAAATTCATTCATTCAGGTAT 466  
Db 121 GlnCysValSerValLeuValSerThrLeuileLeuileSerIleAlaileValArgTyr 140  
Qy 467 CATATGATAAAACATCCCATATCTAATAATTTAAACAGCAAAACATGGCTACTTTCTGATA 526  
Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuile 160  
Qy 527 GCTACTGTCTGGACACTAGTGTGTCATCTGTTCTCCCTTCCAGTGTTCACAGTCTT 586  
Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
Qy 587 GTGGAACTTCAAGAAACATTTGTTTCAGCATTTGTCGAGCAGCAGGTATTATGTGTGAG 646  
Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200  
Qy 647 TCATGGCCATCTGATTCATACAGAAATGGCTTTACTATCTCTTTATTTAGTACTAGTAT 706  
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Qy 707 ATTCTGCCCTTACTTTGTCTTACTGTAACTCATCAAGTGTCTGCAAGAGTATAAGCTGT 766  
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Qy 767 GGATTTCCAAAGAAACAGACTTGAAGAAATGAGATGATGATCACTTAACCTTCTCAT 826  
Db 241 GlyLeuSerAsnLysGluAnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260  
Qy 827 CCATCCAAAAAGAGTGGGCTCAGGTGAAACTCTCTGGCAGCAGCATAAATGGAGTATTCA 886  
Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280

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QY 887 TTTCATCAAAACACAGAGAGATATAGCAAGAGACAGCATGTGTACCTGCTCCA 946
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QY 947 GAAGACCTTCTCAAGAGAACCTCCAGATATCTCCAGAAACTTTGGCTGTGAAGA 1006
Db 301 GluArgProSerGlnGluAsnHisSerArgLysLeuProGluAsnPheGlySerValArg 320
QY 1007 AGTCAGCTCTCTTCATCCAGTAAGTTCATACAGGGGTCCCACTGCTTTGAGATAAAA 1066
Db 321 SerGlnLeuSerSerSerSerLysPheLeuProGlyValProThrCysPheGluLeuLys 340
QY 1067 COTGAAGAAATTCAGATGTTTCATGAATTCAGATGAGATGAGATGAGATGAGATGAGAT 1126
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QY 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATGATGATGATGATGATGATGATGAT 1186
Db 361 LysArgSerArgSerValPheTyArgLeuThrLeuLeuLeuValPheAlaValSer 380
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QY 1247 AGGCATTTCAAGTGTGTATGTCATTTGTCATTTGTTGGCATGATGCTGTTGTTGCTT 1306
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QY 1307 AATCCAATCTATATGCTGTTCTTAAATGAGTAAAGCTGATGATGATGATGATGATGAT 1366
Db 421 AsnProIleLeuTyGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuLys 440
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Db 441 HisCysLeuHisMet 445

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RESULT 12

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US-09-235-839-6
; Sequence 6, Application US/09235839
; Patent No. 6207799
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCaleb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; TITLE OF INVENTION: Sequences
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,839
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,118
; FILING DATE: April 8, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,142
; REFERENCE/DOCKET NUMBER: 96,149-C
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (312)913-0001
; TELEFAX: (312)913-0002
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-235-839-6
Alignment Scores:
Pred. No.: 1,34e-263 Length: 445
Score: 2330.00 Matches: 445
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.95% Indels: 0
DB: 3 Gaps: 0
US-09-771-956-4 (1-1406) x US-09-235-839-6 (1-445)
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Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyLysSerSerValAspAspLeu 40
QY 167 CAGTATTTTCTGATGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGAATCTA 226
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QY 287 GGCAATCTGGCCTTTCTGATATCTTGGTGTGCTGTTTGTCTCACCTTTTCACACTGACG 346
Db 81 GlyAsnLeuAlaPheSerAspLeuValValLeuPheCysSerProPheThrLeuThr 100
QY 347 TCTGCTTCTGCTGATGAGTGGATGTTTGGCAAAGTCATGTCATATATATGCTTTCTT 406
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QY 407 CAATGTGCTCAGTTTGGTTTCAACTTTAATTAATCAATTCATGTCAGTGTAT 466
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Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
QY 767 GGATTGTCCACAAAGAAACAGACTTGAAGAAATGAGATGATCAACTTAACTTTTCAT 826
Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
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Db 281 PheileLysLysHisArgArgTySerLysLysThrAlaCysValLeuProAlaPro 300  
Qy 947 GAAAGACCTTCTCAAGAGAACCTCCAGATATCTCCAGAAACTTTGGCTGTGAAGA 1006  
Db 301 GluArgProSerGlnGluAsnHisSerArgLysLeuProGluAsnPheGlySerValArg 320  
Qy 1007 AGTCAGCTCTCTTCATCCAGTAAGTTTCATACAGAGGGTCCCCACTTCTGTGAGATAAAA 1066  
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Qy 1247 AGGCATTTCAAGTTGGTGATTTGTCATTTGTTGGTCATGATGCTGCTGTGCTT 1306  
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Qy 1367 CACTGTCTTCATATG 1381  
Db 441 HisCysLeuHisMet 445

US-09-327-035-6  
Sequence 6, Application US/09327035  
Patent No. 636824  
GENERAL INFORMATION:  
APPLICANT: Hu Ph.D., Yinghe  
McCaleb Ph.D., Michael L.  
Bloomquist Ph.D., Brian T.  
Flores-Riveros Ph.D., Jaime R.  
Cornfield Ph.D., Linda J.  
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid Sequences  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/327,035  
FILING DATE: 07-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/838,399  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Greenfield Ph.D., Michael S.

REGISTRATION NUMBER: 37,147  
REFERENCE/DOCKET NUMBER: 96,149/WH 405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)715-1000  
TELEFAX: (312)715-1234  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-327-035-6

Alignment Scores:  
Pred. No.: 1,34e-263 Length: 445  
Score: 2330.00 Matches: 445  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.95% Indels: 0  
DB: 3 Gaps: 0

US-09-771-956-4 (1-1406) x US-09-327-035-6 (1-445)

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Qy 167 CAGTATTTCTGATTTGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGAATCTA 226  
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Qy 647 TCATGGCCATCTGATTCATACAGAAATGCTTACTATCTTCTTATTTAGTTCAGTAT 706  
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 Db 441 HisCysLeuHisMet 445

RESULT 14  
 US-09-065-027-2  
 ; Sequence 2, Application US/09065027  
 ; Patent No. 6528303  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Herzog, H.  
 ; TITLE OF INVENTION: NEUROPEPTIDE Y-Y5 RECEPTOR  
 ; FILE REFERENCE: 273402001800  
 ; CURRENT APPLICATION NUMBER: US/09/065,027  
 ; CURRENT FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: PCT/AU96/00706  
 ; PRIOR FILING DATE: 1996-11-08  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 445  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-065-027-2

Alignment Scores:  
 Pred. No.: 1,34e-263 Length: 445  
 Score: 2330.00 Matches: 445  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.95% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-956-4 (1-1406) X US-09-065-027-2 (1-445)

QY 47 ATGGATTTAGAGCTCGACGAGTATTATTAACAAGACACTTGCACAGAGAATAAATCTCT 106  
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 QY 287 GGCMACTCGCCCTTTCTGATATCTGTTGTGTGCTGTTTGTCTCACCTTTTCACACTGACG 346  
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 QY 407 CAATGTGTCTAGTGTGTTTCACTTTAAATTTAAATCAATGCAATGTCAGGTAT 466  
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 QY 467 CATATGATAAAACATCCCATATCTAATTAATTTAAACAGCAAAACATGGGTACTTCTGATA 526  
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 QY 527 GCTACTGTCTGACACTAGTGTGCTTCCATCTCTTCTCCCTTCCAGTGTTCACAGTCTT 586  
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
 QY 587 GTGGAACCTTCAAGAAACATTTGGTTTCAAGTGTGTCAGCAGCAGGTATTTATGCTTTCAG 646  
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200  
 QY 647 TCATGGCCATCTGATTCATACAGAAATGCTTTTACTATCTCTTTTATGCTAGTTCAGTAT 706  
 Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220  
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 QY 767 GGATTTGTCCACAAAACAGACTTGAAGAAAATGAGATGATCAACTTAATCTTTCAT 826  
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260  
 QY 827 CCATCCAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCCATAAATGGAGTTATCA 886  
 Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerLysSer 280  
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 Db 281 PheIleLysLysHisArgArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
 QY 947 GAAAGACCTTCTCAAGAGAACACCTCCAGATATCTCCAGAAAACCTTGGCTCTGTAAGA 1006  
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 QY 1067 CQTGAAGAAAATTCAGATGCTTCATGAATTGAGAGTAAACAGTCTTGTATCAAGAATAAAA 1126  
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Db 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuLeuValPheAlaValSer 380  
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Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuLeuLeuSerAsn 400  
Qy 1247 AGGCATTTCAAGTTGGTGTTATGTCATTTGTCATTTGTTGGCATGATGTCCTGTGTCTT 1306  
Db 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 420  
Qy 1307 AATCCAATTCATATGGTTTCTTAAATATGGGATTAAGCTGATTTAGTGTCCCTTATA 1366  
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Qy 1367 CACTGTCTTCATATG 1381  
Db 441 HisCysLeuHisMet 445

RESULT 15  
US-09-708-392-13  
; Sequence 13, Application US/09708392  
; Patent No. 6734186  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc  
; APPLICANT: Pfizer Limited  
; APPLICANT: Wayman, Chris  
; APPLICANT: Maw, G  
; TITLE OF INVENTION: Pharmaceutical  
; FILE REFERENCE: PC10343AKW  
; CURRENT APPLICATION NUMBER: US/09708,392  
; CURRENT FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: GB 9926437.6  
; PRIOR FILING DATE: 1999-11-08  
; PRIOR APPLICATION NUMBER: GB 0004021.2  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: GB 0013001.3  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 0016563.9  
; PRIOR FILING DATE: 2000-07-05  
; PRIOR APPLICATION NUMBER: GB 0017141.3  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/175,161  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 60/192,962  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/217,479  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: US 60/221,014  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: US 60/221,093  
; PRIOR FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-708-392-13

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Qy 107 GCACCTCGGAATCTGANTTCCAGTCTGGGATGACTATAAAGCAGTGTAGTACTT 166  
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Qy 227 CTTATTTTAAATGGCTCTCATGAAAGCGTATACAGAGACTACGGTAAACCTCTCAT 286  
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Qy 287 GGCATCTCGCTCTTTCTCATATCTTGGTGTGCTGTTTGTCTCACCTTTACACTGAGC 346  
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Qy 347 TCTGTCTCTGTCAGTGCATGTTGGCAAGTCATGTGCCATATATATGCTTTCTT 406  
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120  
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Qy 767 GATTTGTCACAAAGAAACAGACTTGAAGAAATGAGATGATCAACTTACTCTTCA 826  
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| QY | 1187 | TGGATGCCACTACACCTTTTCATGTTGGTAACTGATTTTAATGACAATCTTATTCAAAT  | 1246 |
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| QY | 1247 | AGGCATTTCAAGTTGGTGATATTGCATTTGTCATTTGTTGGGCATGATGTCCTGTGTCTT | 1306 |
| Db | 401  | ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLeu    | 420  |
| QY | 1307 | AATCCAATTCATATGGGTTTCTTAATAAATGGGATTAAAGCTGATTTAGTGTCCTTATA  | 1366 |
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Search completed: October 21, 2004, 12:01:22  
Job time : 65 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 21, 2004, 11:40:49 ; Search time 186 Seconds

(without alignments)  
4894.673 Million cell updates/sec

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Perfect score: 2480

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Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 2729282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2\_1/USPTO\_spool/p/US09771956/runat\_21102004\_103739\_9430/app\_query.fasta\_1.1543

-DB=published Applications AA -QFMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1

-LOPEXT=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=ptc -THR MAX=100

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA:

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
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|            |       |             |           |    |             |

Alignment Scores:

Pred. No.:

Score:

3.11e-223

2385.00

Length:

Matches:

455

455

#### ALIGNMENTS

##### RESULT 1

US-09-771-956-13

; Sequence 13, Application US/09771956

; Patent No. US20010031474A1

; GENERAL INFORMATION:

; APPLICANT: Bennett, Michele

; APPLICANT: Brodbeck, Robbin

; APPLICANT: Krause, James

; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors

; FILE REFERENCE: N2000.001

; CURRENT APPLICATION NUMBER: US/09/771,956

; CURRENT FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 455

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-771-956-13





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 Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleValHisProIleSerAsnAsn 160  
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 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle 180  
 QY 557 TGTCTCCCTCCAGTGTTCACAGTCTTGTGAACCTTCAAGAAACATTTGGTTTCAGCA 616  
 Db 181 CysSerProLeuProValPheHisSerLeuValGlnLeuGlnGluThrPheGlySerAla 200  
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 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260  
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RESULT 4  
 US-10-410-648-7  
 ; Sequence 7, Application US/10410648  
 ; Publication No. US20040072847A1

; GENERAL INFORMATION:  
 ; APPLICANT: Bakthavatchalam, Rajagopal  
 ; APPLICANT: Blum, Charles A.  
 ; APPLICANT: Brielmann, Harry L.  
 ; APPLICANT: Darrow, James W.  
 ; APPLICANT: De Lombaert, Stephanie W.  
 ; APPLICANT: Hutchinson, Alan W.  
 ; APPLICANT: Tran, Jennifer W.  
 ; APPLICANT: Zheng, Xiaozhang W.  
 ; APPLICANT: Elliott, Richard L.  
 ; APPLICANT: Hammond, Marlys L.  
 ; TITLE OF INVENTION: SPIROISOBNZOFURAN-1,4'-PIPERIDIN-3-ONES AND  
 ; FILE REFERENCE: U 014539-7  
 ; CURRENT APPLICATION NUMBER: US/10/410,648  
 ; PRIOR FILING DATE: 2003-04-09  
 ; PRIOR APPLICATION NUMBER: 10/013,846  
 ; PRIOR FILING DATE: 2001-12-11  
 ; PRIOR APPLICATION NUMBER: 60/254,990  
 ; PRIOR FILING DATE: 2000-12-12  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 455  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 ; US-10-410-648-7

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QY 557 TGTTCTCCCTTCAGTGTGTTTCACAGTCTTGTCGAACTTCAAGAAACATTTGGTTACGCA 616
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Db 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240

QY 737 CATCAAGTGTCTCCAGAGTATAAGCTGTGATTGTCTCAACAAAGAAACACAGACTTGAA 796
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; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 30
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; TYPE: PRT
; ORGANISM: Cercopithecus aethiops
US-09-771-956-30

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Query Match: 95.69% Indels: 0
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Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180

QY 557 TGTTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACTTCAAGAAACATTTTGGTTACGCA 616
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QY 617 TTGCTGAGCAGCAGGTATTTATGTTGTGAGTCAATGGCCATCTGATTCATACAGAAATGGC 676
Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220

QY 677 TTACTATCTCTTTATGCTAGTTAGTACATATATCTGCGCTTAGTTGTCTTACTGTAAGT 736
Db 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240

QY 737 CATCAAGTGTCTCCAGAGAGTATAAGCTGTGATTGTCTCAACAAAGAAACACAGACTTGAA 796
Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260

QY 797 GAAATGAGATGATCAACTTAACCTTCTATCCATCCAAAAGAGTGGGCCCTCAGGTGAAA 856
Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerArgLysIleGlyProGlnValLys 280

QY 857 CTCTCTGCAGCCATAAATGAGTATTCTATCATCAAAAACACAGAGAAGATATAGC 916
Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgGlyrSer 300

```

QY 917 AAGAGACAGCATGCTGTTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA 976  
 Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320  
 QY 977 ATACTCCAGAAAACCTTTGGCTCTGTGAAGAAGTCAAGTCTCTTCCATCCAGTAAGTTCATA 1036  
 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340  
 QY 1037 CCAGGGTCCCACTGCTGTTTTCAGATAAAACCTCAAGAAATTCAGATGTCATGAATTG 1096  
 Db 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360  
 QY 1097 AGAGTAAACGTTCTGTTTACAGAAATAAAAGAGATCTCGAAGTGTGTTTCTACAGACTG 1156  
 Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380  
 QY 1157 ACCATACTGATATTAGTATTGCTGTGTAGTTGGATGGACACACACCTTTCCATGGTA 1216  
 Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400  
 QY 1217 ACTGATTTTAAATGACAATCTATTTCAAATAGGCATTTCAAGTTGGTGTATTGCAATTTGT 1276  
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420  
 QY 1277 CATTTGTTGGGCATGATGCTGCTGTTGTCTTAATCCAATTCATATGGGTTTCTTAATAAT 1336  
 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
 QY 1337 GGGATTAAGTCATTTAGTGTCCCTTATACACACTGCTTCATATG 1381  
 Db 441 GlyIleLysAlaAspLeuMetSerLeuIleHisCysLeuHisMet 455

RESULT 6  
 US-10-274-851-7  
 ; Sequence 7, Application US/10274851  
 ; Publication No. US20030144290A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blum, Charles  
 ; APPLICANT: Brielmann, Harry  
 ; APPLICANT: De Lombaert, Stephane  
 ; APPLICANT: Zheng, Xiaozhang  
 ; TITLE OF INVENTION: SUBSTITUTE 2-CYCLOHEXYL-4-PHENYL-1H-IMIDAZOLE  
 ; TITLE OF INVENTION: DERIVATIVES  
 ; FILE REFERENCE: U 014209-8  
 ; CURRENT APPLICATION NUMBER: US/10/274,851  
 ; CURRENT FILING DATE: 2002-10-21  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 455  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-274-851-7

Alignment Scores:  
 Pred. No.: 1,41e-221 Length: 455  
 Score: 2368.00 Matches: 453  
 Percent Similarity: 99.56% Conservative: 0  
 Best Local Similarity: 99.56% Mismatches: 2  
 Query Match: 95.48% Indels: 0  
 DB: 14 Gaps: 0

US-09-771-956-4 (1-1406) x US-10-274-851-7 (1-455)

QY 17 ATGCTTTTATTCACAGCAGCATATAATATGATTTAGCTCGCAGAGTATTATAAC 76  
 Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20  
 QY 77 AAGACACTTGCACAGAAATAACTGCTGCCACTCGGAATTCGGAATTCGATTTCCCACTGCG 136  
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40

QY 137 GATGACTATAAAAGCAGTGTAGATGACTTACAGTATTTTCTGATTGGGCTCTATACATTT 196  
 Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60  
 QY 197 GTAAGTCTTTGGCTTTATGGGAAATCTACTATTATTTAAATGGCTCTCATGAAAAGCGT 256  
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80  
 QY 257 AATCAGACACTACGTAACCTTCTCATAGGCAATCTGGCCTTTCTTGATATCTTGTT 316  
 Db 81 AsnGlnLysThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100  
 QY 317 GTGCTGTTTGTCTCACTTTTCACTACGCTGCTGCTTCTGCTGGATCAGTGAATGTTGGC 376  
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120  
 QY 377 AAGATCATGTGCATATTATAGCTTTTCTCAATGTGTCTAGTGTCTGCTTTGGTTCACTTTA 436  
 Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140  
 QY 437 ATTTTAAATCAATTCGCCATTTGTCAGGTATCATATGATAAAACATCCCATATCTAATAAT 496  
 Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160  
 QY 497 TTAACAGCAACCATGGCTACTTTCTGATAGCTACTGCTGCTGACACTAGGTTTGGCCATC 556  
 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180  
 QY 557 TGTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACCTCAAGAAACATTTGGTTTCAGCA 616  
 Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200  
 QY 617 TTGCTCAGCAGCAGTATTATGCTTCAAGTCATGCGCATCTGATCTATACAGAAATGCC 676  
 Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220  
 QY 677 TTTACTATCTCTTTATGCTAGTTCAGTATATTCGCGCTTAGTTGCTTACTGTAGT 736  
 Db 221 PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240  
 QY 737 CATCAAGTGTCTGCAGAAAGTATAAGCTGTGGATTTGTCCAAACAAAGAAACAGACTTGAA 796  
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerTrpLysGluAsnArgLeuGlu 260  
 QY 797 GAAATGAGATGATCAACTTAACCTTCTCATCCATCCAAAAGAGTGGCGCTCAGGTGAA 856  
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280  
 QY 857 CTCTCTGGCAGCCATAAATGGAGTTTATTTCATTTCATCAAAAACACAGAAAGATATAGC 916  
 Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300  
 QY 917 AAGAAGACAGCATGTGTGTTACCTCTCCAGAAAGACCTTCTCAAGAAACACACTCCAGA 976  
 Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320  
 QY 977 ATACTTCCAGAAAACCTTTGGCTCTGTAAGAAGTCAAGCTCTCTTCATCCAGTAAGTTCATA 1036  
 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340  
 QY 1037 CCAGGGTCCCACTGCTGTTTTCAGATAAAACCTGAAGAAATTCAGATGTTTCATGAATTG 1096  
 Db 341 ProGlyValProThrCysPheGluIleLeuProGluGluAsnSerAspValHisGluLeu 360  
 QY 1097 AGAGTAAACGTTCTGTTTACAGAAATAAAAGAGATCTCGAAGTGTGTTTCTACAGACTG 1156  
 Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380  
 QY 1157 ACCATACTGATATTAGTATTGCTGTGTAGTTGGATGGCACTACACCTTTCCATGGTA 1216  
 Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400  
 QY 1217 ACTGATTTTAAATGACAATCTATTTCAAATAGGCAATTCAGTGTGGTGTATTGCAATTTGT 1276

Db 401 ThrAspPheAsnAspAsnLeuLeuSerAsnArgHisPheLysLeuValTyrCysIleCys 420  
 Qy 1277 CATTTGTTGGCAGTANGTCTGTGTTCTTAATCCCAATTTCTATATGGGTTTCTTAATAAT 1336  
 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440  
 Qy 1337 GGGATTAAAGCTGATTAGTGTCCCTTATACACTGCTTTCATATG 1381  
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 7  
 US-10-027-049-6  
 ; Sequence 6, Application US/10027049  
 ; Publication No. US20030022283A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hu Ph.D., Yinghe  
 ; McCaleb Ph.D., Michael L.  
 ; Bloomquist Ph.D., Brian T.  
 ; Flores-Riveros Ph.D., Jaime R.  
 ; Cornfield Ph.D., Linda J.  
 ; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
 ; Sequences  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
 ; STREET: 300 South Wacker Drive, 32nd Floor  
 ; CITY: Chicago  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/027,049  
 ; FILING DATE: 08-Apr-1996  
 ; CLASSIFICATION: <unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Greenfield Ph.D., Michael S.  
 ; REGISTRATION NUMBER: 37,142  
 ; REFERENCE/DOCKET NUMBER: 96,149/WH 405  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312) 715-1000  
 ; TELEFAX: (312) 715-1234  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 445 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-10-027-049-6

Qy 167 CAGTATTTCTGATTGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGAATCTA 226  
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 Qy 227 CTTATTTTAATGGCTCTCATGAAGAAGGTAAATCAGAGACTACCGTAACTTCCTCAT 286  
 Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuIle 80  
 Qy 287 GGCAATCTGGCCCTTTTCTGATATCTTGGTGTGCTGTTTGTCTCACCTTTTCACACTG 346  
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100  
 Qy 347 TCTGCTCTCTGATCAGTGGATGTTTGGCAAGACATGTGCCATATATATGCTTTCTT 406  
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120  
 Qy 407 CAATGTGTCTCAGTGTGTTTGGTTTCAACTTTAAATATCAATTCACATTCAGGTAT 466  
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140  
 Qy 467 CATATGATAAAACATCCCATATCTAATAATTAAACAGCAACCCATGGCTACTTCTGATA 526  
 Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160  
 Qy 527 GCTACTGTCTGGACACTAGGTTTTCCTCTCTCTCCCTTCCAGTGTTCACAGTCTT 586  
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
 Qy 587 GTGGAACTTCAAGAAACATTTGTTTTCAGCATTCGACAGCAGGTATTTATGTGTGAG 646  
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200  
 Qy 647 TCATGGCCATCTGATTTCATACAGAAATTCCTTACTATCTCTTATTTGCTAGTCTCAGTAT 706  
 Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220  
 Qy 707 ATTCTGCCCTTAGTTTGTCTTACTGTAGTCTACAAAGTGTCTGCAGAGTATAAGTCT 766  
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
 Qy 767 GATTTCTCAACAAAGAAACAGACTTGAAGAAATAGATGATCAACTTACTCTTCT 826  
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260  
 Qy 827 CCATCCAAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCCATAAATGGAGTTATCA 886  
 Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280  
 Qy 887 TTCATCAAAAAACACAGAAAGATATAGCAAGAGACAGCATGTGTGTACTCTCTCCA 946  
 Db 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
 Qy 947 GAAGACCTTCTCAAGAGAACCACTCCAGAACTCTCCAGAAACCTTTGGCTCTGTAAGA 1006  
 Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlyValArg 320  
 Qy 1007 AGTCAGCTCTCTTCATCCAGTAAGTTTCATACAGGGGTCCCACTTGTCTTGGAGATAAAA 1066  
 Db 321 SerGlnLeuSerSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340  
 Qy 1067 CTTGAAGAAAAATTCAGATGTTTCATGAATTCAGAGTAAACCGTCTGTTTCACAGAATAAAA 1126  
 Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360  
 Qy 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTATATAGTATTTGCTGTAGT 1186  
 Db 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleValPheAlaValSer 380  
 Qy 1187 TGGATCCCACTACACCTTTTCCATGTTGTTAACTGATTTTAAATGACAACTTATTTCAAT 1246  
 Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400

Alignment Scores:  
 Pred. No.: 7,03e-218 Length: 445  
 Score: 2330.00 Matches: 445  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.95% Indels: 0  
 DB: 14 Gaps: 0

US-09-771-956-4 (1-1406) x US-10-027-049-6 (1-445)

Qy 47 ATGGATTTAGAGTCGACGATATATATACAGACACTTGCACAGAGATATATCTGCT 106  
 Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20  
 Qy 107 GCCACTCCGAATTTCTGATTTCCCACTTGGGATGACTATAAAGCAGTGTAGATGACTTA 166  
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspLeu 40

QY 1247 AGGCATTTCAAGTGGTGGTATGATTTGTGATTTGTGGCATGATGCTCTGTGTCTT 1306  
 |||||  
 Db 401 ArgHisPheLysLeuValTy-CysIleCysHisLeuLeuGlyMetMetSerCysLeu 420  
 |||||  
 QY 1307 AATCAATTTCTATATGGTGTCTTTAAATAATGGGATTAAGAGTGATTTAGTGTCCCTTATA 1366  
 |||||  
 Db 421 AsnProIleLeuTyGlyPheLeuAsnGlnGlyIleLysAlaAspLeuValSerLeuLeu 440  
 |||||  
 QY 1367 CACTGTCTTCATATG 1381  
 |||||  
 Db 441 HisCysLeuHisMet 445  
 |||||

## RESULT 8

US-10-225-567A-205  
 ; Sequence 205, Application US/10225567A  
 ; Publication No. US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LifeSpan Biosciences  
 ; APPLICANT: Brown, Joseph P.  
 ; APPLICANT: Burner, Glenn C.  
 ; APPLICANT: Roush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 ; FILE OF INVENTION: 1920-4-4  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; PRIORITY FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,144  
 ; PRIOR FILING DATE: 2000-12-19  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 205  
 ; LENGTH: 445  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-225-567A-205

## Alignment Scores:

Pred. No.: 7,03e-218 Length: 445  
 Score: 2330.00 Matches: 445  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.95% Indels: 0  
 DB: 14 Gaps: 0

US-09-771-956-4 (1-1406) x US-10-225-567A-205 (1-445)

QY 47 ATGATTTAGAGCTCGACGAGTATATATAACAAGACACTTGGCCACAGAGAATAATACTGCT 106  
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 Db 1 MetAspLeuGluLeuAspGluTy-TyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20  
 |||||  
 QY 107 GCCACTCGGAATTCGATTTCCAGTCTGGGATGACTATATAAAGCAGCTGTAGATGACTTA 166  
 |||||  
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyLysSerSerValAspAspLeu 40  
 |||||  
 QY 167 CAGTATTTCTGATGGCTCTATACATTTGTAGTCTTCTTGCTTTATGGGAATCTA 226  
 |||||  
 Db 41 GlnTyPheLeuIleGlyLeuTyPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 |||||  
 QY 227 CTTATTTTAAATGGCTCTCATGAAAGCGTAATCAGAAGACTACGGTAAACTTTCCTCATA 286  
 |||||  
 Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeuLeu 80  
 |||||  
 QY 287 GGCATCTGGCTTTCTGATATCTTGGTGTGCTGTGTTGCTTCACCTTTCACACTGACG 346  
 |||||  
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100  
 |||||  
 QY 347 TCTGCTTCTGGATCAGTGTGATTTGGCAAGTCATGTGCCATATATATGCCCTTTTCTT 406  
 |||||  
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120  
 |||||  
 QY 407 CAATGTGTGCTAGTTTGGTTTCAACTTAAATTTTAAATATATCAATGGCATGTGCTAGTAT 466  
 |||||  
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTy 140  
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QY 467 CATATGATTAACATCCCATATCTCTAATAATTTAAGCAGCAACCATGGCTACTTCTTGATA 526  
 |||||  
 Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyPheLeuLeu 160  
 |||||  
 QY 527 GCTACTGTCTGACACTAGGTTTCCCATCTGTTCTCCCTTCCAGTGTTCACAGTCTT 586  
 |||||  
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
 |||||  
 QY 587 GTGGAATTTCAAGAAACATTTGGTTCAGCATTTCTGACGACGAGGTATTTATGTTGAG 646  
 |||||  
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyLeuCysValGlu 200  
 |||||  
 QY 647 TCATGGCCATCTGATTCATACAGAAATTCCTTACTATCTCTTATTCTAGTTCAGTAT 706  
 |||||  
 Db 201 SerTrpProSerAspSerTyArgIleAlaPheThrIleSerLeuLeuLeuValGlnTy 220  
 |||||  
 QY 707 ATTCTGCCCTTAGTTTGTCTTACTCTAAGTCTATACAAGTGTCTGACAGATTAAGCTGT 766  
 |||||  
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
 |||||  
 QY 767 GSATTTCTCCAAAGAAACAGACTTGAAGAAATGAGATGATCAACTTAACCTTTCAT 826  
 |||||  
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluAsnGluMetIleAsnLeuThrLeuHis 260  
 |||||  
 QY 827 CCATCCAAAAGAGTGGGCTCAGGTGAAACTCTCTGGCAGCCATAAATGGAGTTATTCA 886  
 |||||  
 Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTySer 280  
 |||||  
 QY 887 TTCATCAAAAACACAGAAGAAGATATAGCAAGACAGAGATGCTGTACCTGCTCCA 946  
 |||||  
 Db 281 PheIleLysLysHisArgArgTySerLysLysThrAlaCysValLeuProAlaPro 300  
 |||||  
 QY 947 GAAAGACCTTCTCAAGAGAACCCACTCCAGATACTTCCAGAAACCTTGGCTCTGTAGA 1006  
 |||||  
 Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320  
 |||||  
 QY 1007 ACTCAGCTCTCTTCATCCAGTAAGTTTCATACAGGGGTCCTGCTTTGAGATAAAA 1066  
 |||||  
 Db 321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340  
 |||||  
 QY 1067 CCTGAAGAAATTCAGATGTTTCATGAATGAGAGTAAACGTTCTGTACAGAAATAAA 1126  
 |||||  
 Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360  
 |||||  
 QY 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATGACTGATATTAGTATTGCTGTAGT 1186  
 |||||  
 Db 361 LysArgSerArgSerValPheTyArgLeuThrIleLeuIleLeuValPheAlaValSer 380  
 |||||  
 QY 1187 TGGATGCCACTACACTTTTCCATGTTGTAAGTATTTAATGACAATCTTATTCAAT 1246  
 |||||  
 Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400  
 |||||  
 QY 1247 AGGCATTTCAAGTGTGCTATTGCAATTTCTCATTTTGGGCATGATCTCTGTGTCTT 1306  
 |||||  
 Db 401 ArgHisPheLysLeuValTyCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 420  
 |||||  
 QY 1307 AATCAATCTATATGGGTTTCTTAAATATGGGATTAAGCTGATTTAGTCTCCCTTATA 1366  
 |||||  
 Db 421 AsnProIleLeuTyGlyPheLeuAsnGlnGlyIleLysAlaAspLeuValSerLeuLeu 440  
 |||||  
 QY 1367 CACTGTCTTCATATG 1381  
 |||||  
 Db 441 HisCysLeuHisMet 445  
 |||||

## RESULT 9

US-10-295-027-668  
 ; Sequence 668, Application US/10295027  
 ; Publication No. US20030232350A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Afar, Daniel  
 ; APPLICANT: Aziz, Natasha  
 ; APPLICANT: Ginsberg, Wendy M.  
 ; APPLICANT: Gish, Kurt C.



APPLICANT: Glynn, Richard  
 APPLICANT: Hevezi, Peter A.  
 APPLICANT: Mack, David H.  
 APPLICANT: Murray, Richard  
 APPLICANT: Watson, Susan R.  
 APPLICANT: Eos Biotechnology, Inc.  
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
 TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
 FILE REFERENCE: 018501-01250005  
 CURRENT APPLICATION NUMBER: US/10/295,027  
 CURRENT FILING DATE: 2002-11-13  
 PRIOR APPLICATION NUMBER: US 09/663,733  
 PRIOR FILING DATE: 2000-09-15  
 PRIOR APPLICATION NUMBER: US 60/350,666  
 PRIOR FILING DATE: 2001-11-13  
 PRIOR APPLICATION NUMBER: US 60/335,394  
 PRIOR FILING DATE: 2001-11-15  
 PRIOR APPLICATION NUMBER: US 60/332,464  
 PRIOR FILING DATE: 2001-11-21  
 PRIOR APPLICATION NUMBER: US 60/334,393  
 PRIOR FILING DATE: 2001-11-29  
 PRIOR APPLICATION NUMBER: US 60/340,376  
 PRIOR FILING DATE: 2001-12-14  
 PRIOR APPLICATION NUMBER: US 60/347,211  
 PRIOR FILING DATE: 2002-01-08  
 PRIOR APPLICATION NUMBER: US 60/347,349  
 PRIOR FILING DATE: 2002-01-10  
 PRIOR APPLICATION NUMBER: US 60/355,250  
 PRIOR FILING DATE: 2002-02-08  
 PRIOR APPLICATION NUMBER: US 60/356,714  
 PRIOR FILING DATE: 2002-02-13  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 1386  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 668  
 LENGTH: 445  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-295-027-668

Alignment Scores:  
 Pred. No.: 7,03e-218 Length: 445  
 Score: 2330.00 Matches: 445  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 93.95% Indels: 0  
 DB: 14 Gaps: 0

US-09-771-956-4 (1-1406) x US-10-295-027-668 (1-445)  
 QY 47 ATGGATTAGAGTCGACGATATTATACAAAGACACTTCCACAGAGATAATACTGCT 106  
 DB 1 MetAspLeuGluLeuAspGluTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20  
 QY 107 GCCACTCGGANTCTGATTTCCAGTCTGGGATGACTATAAAGCAGTGTAGATGACTTA 166  
 DB 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40  
 QY 167 CAGTATTTCGATTGGGCTCTATACATTTGTAAGTCTTCTGGCTTTTATGGGGAATCTA 226  
 DB 41 GlnTyrPheLeuLeuGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 QY 227 CTTATTTTAATGGCTCTCATGAAAGCGTAATCAGAGACTACGGTAAGACTTCTCTCAT 286  
 DB 61 LeuileLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeu 80  
 QY 287 GGCAATCTGGCTTTCTGATATCTTGGTGTGCTGTTTGTCTCACCTTTCCACTGACG 346  
 DB 81 GlyAsnLeuAlaPheSerAspLeuValValLeuPheCysSerPropheThrLeuThr 100  
 QY 347 TCTGCTTCGTGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 406  
 DB 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetPropheLeu 120

QY 407 CAATGTGTGTCAGTTCGTTTGGTTTCACTTAAATTTTAAATATCAATTCGCTAGGTAT 466  
 DB 121 GlnCysValSerValLeuValSerThrLeuLeuLeuSerIleAlaIleValArgTyr 140  
 QY 467 CATATGATAAAACATCCCATATCTAATAATTAACAGCAAAACCATGGCTACTTTCTGATA 526  
 DB 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuLeu 160  
 QY 527 GCTACTGTGTCGACACTAGGTTTCCCATCTGTTCTCCCTTCCAGTGTTCACAGTCTT 586  
 DB 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
 QY 587 GTGGAACCTTCAAGAAACATTTGGTTTCACTTGTGAGCAGCAGGATTTATGTCTTCCAG 646  
 DB 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200  
 QY 647 TCATGCCCATCTGATTTCATACAGAAATGCTTTACTATCTCTTTTACTGCTAGTTCAGTAT 706  
 DB 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220  
 QY 707 ATCTGCTCCCTTAGTTTGTCTTACTGCTAGTATACAGTCTGTCAGAGATATAAGTGT 766  
 DB 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
 QY 767 GGATTGTCCAAACAAAGAAACACAGACTTGAAGAAATGAGATGATCAACTTAACTTCTCAT 826  
 DB 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260  
 QY 827 CCATCCAAAGAGTGGGCTCAGTGAACTCTCTGCGAGCCATATAATGGAGTTATCA 886  
 DB 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280  
 QY 887 TTCATCAAAACACAGAAAGATATACAGAAAGACAGATGCTGTGTACTCTCTCTCTCA 946  
 DB 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
 QY 947 GAAAGACCTTCTCAAGAGAACCCACTCCAGATATCTCCAGAAACATTTGGCTCTCTGTA 1006  
 DB 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320  
 QY 1007 AGTCAGCTCTTTCATCCAGTAAGTTTCATACAGGGGTCCCTTCTTTCAGATATAAA 1066  
 DB 321 SerGlnLeuSerSerSerSerLysPheIleProGlyValProThrCysPheGluLeuLys 340  
 QY 1067 CCTGAAGAAATTCAGATGTTTCATGAATTCAGAGTAAACCGTTCTGTGTACAGAAATAAA 1126  
 DB 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgileLys 360  
 QY 1127 AGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTGATATTAGTATTGCTGTTAGT 1186  
 DB 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuLeuValPheAlaValSer 380  
 QY 1187 TGGATGCCACTACACCTTTTCCATGTGTAACCTGATTTTAAATGCAATCTTATTTCAAT 1246  
 DB 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400  
 QY 1247 AGCATTTCAAGTTGGTGTGATTTGCAATTTGTCATTTGTTGGGATGATGCTCTGTGCTT 1306  
 DB 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 420  
 QY 1307 AATCCAAATCTATATGGGTTTCTTAAATATGGATTAAAGCTGATTAGTGTCCCTTATA 1366  
 DB 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuLeu 440  
 QY 1367 CACTGTCTTTCATATG 1381  
 DB 441 HisCysLeuHisMet 445

RESULT 10  
 US-10-181-906-14  
 ; Sequence 14, Application US/10181906  
 ; Publication No. US20040053864A1

```

; GENERAL INFORMATION:
; APPLICANT: Karsenty, Gerard
; APPLICANT: Amling, Michael
; APPLICANT: Ducey, Patricia
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA
; TITLE OF INVENTION: MODULATION OF NEUROPEPTIDE Y ACTIVITY
; FILE REFERENCE: 9142-020-999
; CURRENT APPLICATION NUMBER: US/10/181.906
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/02040
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-181-906-14

Alignment Scores:
Pred. No.: 7.03e-218 Length: 445
Score: 2330.00 Matches: 445
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.95% Indels: 0
DB: 15 Gaps: 0

US-09-771-956-4 (1-1406) x US-10-181-906-14 (1-445)
QY 47 ATGGATTAGAGCTCGACGAGTATTATAACAGACACTTGCACAGAGAATAATACTGCT 106
DB 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
QY 107 GCCACTCGGAATTCGATTTCCGATCTGGGATCGGATCACTATAAAGCAGGTAGACTTA 166
DB 21 AlaThrArgAsnSerAspPheProValTyrAspAspTyrLysSerSerValAspAspLeu 40
QY 167 CAGTATTTCTGATTGGGCTCTATACATTTCTTAAGTCTCTTGGCTTTATGGGAATCTA 226
DB 41 GlnTyrPheLeuLeuGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
QY 227 CTTATTTAATGGCTCTCATGAAAGCGTAAATCAGAAGACTACGGTAAACTTCTCTCAT 286
DB 61 LeuLeuLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeuLe 80
QY 287 GGCAATCTGGCTTTCTGATATCTTGGTGTGCTGTTTCTCACCTTTACACTGACG 346
DB 81 GlyAsnLeuAlaPheSerAspLeuLeuValValLeuPheCysSerProPheThrLeuThr 100
QY 347 TCTGCTTCTGGATCAGTGGATGTTTGGCAAGTCACTGTGCCATATTATGCTTTTCTT 406
DB 101 SerValLeuLeuAspGlnTyrMetPheGlyLysValMetCysHisLeuMetProPheLeu 120
QY 407 CAATGTGTCTCAGTTTGGTTTCACTTTAATTTAATATCAATTCATGTCAGGTAT 466
DB 121 GlnCysValSerValLeuValSerThrLeuLeuLeuLeuSerLeuAlaLeuValArgTyr 140
QY 467 CATATGATAAAACATCCCATATCAATAAATTTAAACAGCAAAACCATGCTACTTCTGATA 526
DB 141 HisMetLeuLysHisProLeuSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuLe 160
QY 527 GCTACTGTCTGGACACTAGGTTTGGCATCTGTTCTCCCTTCCAGTGGTTTCACAGCTT 586
DB 161 AlaThrValTyrThrLeuGlyPheAlaLeuLeuCysSerProLeuProValPheHisSerLeu 180
QY 587 GTGGAATCTCAAGAAACATTTGGTTTGCAGCATTTGCTGAGCAGCAGATTTATGTGTGAG 646
DB 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
QY 647 TCATGGCCATCTGATTCATACAGAAATGCGCTTTACTATCTCTTTATGCTAGTTTCAGTAT 706
DB 201 SerTyrProSerAspSerTyrArgLeuAlaPheThrLeuSerLeuLeuValGlnTyr 220

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QY 707 ATTTCGCCCTTAGTTTGTCTTACTGTAACTCATACAAAGTGTCTGCAGAAAGTATAAGCTGT 766
DB 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
QY 767 GGATGTTCACAAAGAAACAGACTTGAAGAAAATGAGATGATCAACTTAACCTTCTTCA 826
DB 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
QY 827 CCATCCAAAAGAGTGGGCTCAGGTGAAACTCTTCGACGCCATAAATGAGTTTATTC 886
DB 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTyrSerTyrSer 280
QY 887 TTCATCAAAAACACAGAGAGATATACAGAGAGAGAGATGCTGTGTACCTGCTCCA 946
DB 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
QY 947 GAAAGACCTTCTCAAGAGAACCACTCCAGATACTTCCAGAAAACCTTTGGCTCTGTAAGA 1006
DB 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
QY 1007 AGTCAGCTCTCTTCATCCAGTAAGTTTCATACAGAGGGTCCCCACTGCTTTGAGATAAAA 1066
DB 321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluLeuLys 340
QY 1067 CCTGAAGAAAATTCAGATGCTTCATGAATTGAGAGTAAACCGTTCTGTTCACAGAAATAAAA 1126
DB 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360
QY 1127 AAGAGATCTCGAAGTGTCTTTCTACAGACTGACCATCTATATAGTATTGCTGTTAGT 1186
DB 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuLeuValPheAlaValSer 380
QY 1187 TGGATGCCACTACACTTTTCCATGCTGTAAGTAACTGATTTTAAATGACAACTTATTTCAAAT 1246
DB 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuLysSerAsn 400
QY 1247 AGGCATTTCAAGTGTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1306
DB 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 420
QY 1307 AATCCAACTCTATATGCTGCTTCTTAATATCGGATTAAGCTGATTTAGTGTCCCTTATA 1366
DB 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuLe 440
QY 1367 CACTGTCTTCATATG 1381
DB 441 HisCysLeuHisMet 445

RESULT 11
US-09-771-956-9
; Sequence 9, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771.956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Y5/Y1 CHIMERA
US-09-771-956-9

Alignment Scores:
Pred. No.: 1.77e-217 Length: 499
Score: 2326.00 Matches: 444

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Percent Similarity: 99.78%  
 Best Local Similarity: 99.55%  
 Query Match: 93.79%  
 DB: 9

US-09-771-956-4 (1-1406) x US-09-771-956-9 (1-499)

QY 17 ATGCTTTTATTCAGCAGGACTATAATAGGATTTAGAGCTCGAGGATTTATAAC 76  
 DB 1 MetSerPheTySerLysGlnAspTyAsnMetAspLeuGluLeuAspGluTyTyAsn 20  
 QY 77 AAGACATTCGACAGAGAAATAACTGCTGCCACTCGGAATTCGTATTTCCAGTCTGG 136  
 DB 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40  
 QY 137 GATGACTATAAAGCAGGTAGAGTACATTCAGATATTTTCGATGGGCTCTATACATTT 196  
 DB 41 AspAspTyLysSerSerValAspAspLeuGlnTyPheLeuLeuGlyLeuTyThrPhe 60  
 QY 197 GTAAGTCTTCTGCTTTATGGGAATCTACTATTTTAATGGCTCTCATGAAAGCGT 256  
 DB 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuLeuLeuMetAlaLeuMetLysLysArg 80  
 QY 257 AATCAGAGACTACGGTAAACTTCTCATAGGCAATCTGGCTTTTCTGATATCTGGTT 316  
 DB 81 AsnGlnTyThrThrValAsnPheLeuLeuLeuGlyAsnLeuAlaPheSerAspIleLeuVal 100  
 QY 317 GTGCTGTTTCTCACCTTTCACACTGACGCTCTGCTGTCGATCGATGATGTTGGC 376  
 DB 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120  
 QY 377 AAGTCATGTGCCATATTAATGCTTTTCTCAATGTGTGTCAGTGTGTTTCAACTTTA 436  
 DB 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140  
 QY 437 ATTTTAATCAATGCGCATTCAGGTATCATATGATATAAACAATCCCATATCTAAAT 496  
 DB 141 IleLeuIleSerIleAlaIleValArgTyHisMetIleLysHisProIleSerAsnAsn 160  
 QY 497 TTAACAGCAACCATGCTGCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556  
 DB 161 LeuThrAlaAsnHisGlyTyPheLeuLeuAlaThrValThrLeuGlyPheAlaIle 180  
 QY 557 TGTTCTCCCTTCCAGTCTTTTACAGTCTTTTCAAGTCTTTTCAAGTCTTTTCAAGT 616  
 DB 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200  
 QY 617 TTGTCAGCAGCAGGATTTATGCTGTCAGTCATGCTGCTGCTGCTGCTGCTGCTGCT 676  
 DB 201 LeuLeuSerSerArgTyLeuCysValGlnSerTrpProSerAspSerTyArgIleAla 220  
 QY 677 TTTACTATCTCTTATTCTAGTTCAGTATATTCGCTTGTGCTTGTGCTTGTGCTTGT 736  
 DB 221 PheThrIleSerLeuLeuValGlnTyIleLeuProLeuValCysLeuThrValSer 240  
 QY 737 CATCAAGTCTGACAGAGTATAAGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 796  
 DB 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260  
 QY 797 GAAATGATGATGATCACTTAACTTCTCATCATCAAAAGAGTGGGCTTCAGTGAAG 856  
 DB 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280  
 QY 857 CTCTCTGCAGCCTAATAAGGATTTATTCATATCAATAAAGAGAGAGAGATATAGC 916  
 DB 281 LeuSerGlySerHisLysTrpSerTySerPheIleLysLysHisArgArgTySer 300  
 QY 917 AAGAGACAGATGCTGCTACCTGCTCCAGAGAGACCTTCTCAAGAGAACCTCCAGA 976  
 DB 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320  
 QY 977 ATACTTCCAGAAACTTTGGCTCTGTAAGAGAGTTCAGCTCTCTTCTCATCAGTAACTTCATA 1036

DB 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerSerLysPheIle 340  
 QY 1037 CCAGGGTCCCACCTGCTTTCAGATATAAACTGAGAAATTCAGATTTTCATGAATTG 1096  
 DB 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360  
 QY 1097 AGAGTAAACGCTTCTGTTACAAGATATAAAAGAGATCTCGAAGTCTTTTCTACAGACTG 1156  
 DB 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyArgLeu 380  
 QY 1157 ACCATATCTGATATTAATTTCTGTTAGTTCGATGCTGCTGCTGCTGCTGCTGCTGCT 1216  
 DB 381 ThrIleLeuLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400  
 QY 1217 ACTGATTTTAAAGACATCTTATTTCAATAGGCAATTTCAAGTGTGTTATGCTGCTGCT 1276  
 DB 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyCysIleCys 420  
 QY 1277 CATTTCTTGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1336  
 DB 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyGlyPheLeuAsnAsn 440  
 QY 1337 GGGATTTAAAGCTGATTTTA 1354  
 DB 441 GlyIleGlnArgAspLeu 446

RESULT 12

US-09-826-509-533  
 ; Sequence 533, Application US/09826509  
 ; Publication No. US20030204073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lehmann-Bruinsma, Karin  
 ; APPLICANT: Liaw, Chen W.  
 ; APPLICANT: Lin, I-Lin  
 ; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G  
 ; TITLE OF INVENTION: Protein-Coupled Receptors  
 ; FILE REFERENCE: AREN-207  
 ; CURRENT APPLICATION NUMBER: US/09/826,509  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/195,747  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: 09/170,496  
 ; PRIOR FILING DATE: 1998-10-13  
 ; NUMBER OF SEQ ID NOS: 599  
 ; SOFTWARE: Patent In Version 2.1  
 ; SEQ ID NO 533  
 ; LENGTH: 445  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-826-509-533

Alignment Scores:  
 Pred. No.: 5,29e-217 Length: 445  
 Score: 2321.00 Matches: 444  
 Percent Similarity: 99.78% Conservative: 0  
 Best Local Similarity: 99.78% Mismatches: 1  
 Query Match: 93.59% Indels: 0  
 DB: 10 Gaps: 0

US-09-771-956-4 (1-1406) x US-09-826-509-533 (1-445)

QY 47 ATGATTTAGAGCTCGACGAGTATTATAACAAGACACTTCGCCACAGAGATATACTGCT 106  
 DB 1 MetAspLeuGluLeuAspGluTyTyAsnLysThrLeuAlaThrGluAsnAsnThrAla 20  
 QY 107 GCCACTCGGAATTTCTGATTTCCAGTCTGGGATGACTATAAAAGCAGGTAGATGACTTA 166  
 DB 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyLysSerSerValAspAspLeu 40  
 QY 167 CAGTATTTCTGATTTGGGCTCTATACATTTGTAAAGTCTTTCTGGCTTTATGGGATCTTA 226  
 DB 41 GlnTyPheLeuIleGlyLeuTyThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60



455 ATTGTCAGGTATCATATGATAAACAATCCCATATCTAATAATTAACAGCAAAACCATGGC 514  
 148 ILeValArgTyrHisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGly 167  
 515 TACTTTCTGATAGTACTGTGGACACTAGGTTTGGCCATCTGTCTCCCTTCCAGTG 574  
 168 TyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIleCysSerProLeuProVal 187  
 575 TTTCACAGTCTTGTGGAACTCAAGAAACATTTGGTTCAGCATTCGTGACACAGGTAT 634  
 188 PheHisSerLeuValGluLeuLysGluThrPheGlySerAlaLeuSerSerLysTyr 207  
 635 TTATGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 694  
 208 LeuCysValGluSerTyrProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeu 227  
 695 CTAGTTCAGTATATCTGCTGCTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 754  
 228 LeuValGlnTyrIleLeuProLeuValCysLeuThrValSerHisThrSerValCysArg 247  
 755 AGTAAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 814  
 248 SerIleSerCysGlyLeuSerHisLysGluAsnArgLeuGluAsnGluMetIleAsn 267  
 815 TTAATCTTTCATCATCAAAAGAGTGGGCTCAGGTGAACTCTCTGGCAGCCATAAA 874  
 268 LeuThrLeuGlnProSerLysSerArgAsnGlnAlaLysThrProSerThrGlnLys 287  
 875 TGGAGTATTCATTCATCAAAACACAGAGAGATATACAGAGAGAGAGAGAGAGAGAGAG 934  
 288 TrpSerTyrSerPheIleArgLysHisArgArgArgTyrSerLysThrAlaCysVal 307  
 935 TTACTCTGTCAGAAAGACCTTCCAAAGAGAACCTCCAGAAATCTTCCAGAAACCTTT 994  
 308 LeuProAlaProAlaGlyProSerGlnGlyLysHisLeuAlaVal---ProGluAsnPro 326  
 995 GGCTCTGTAGAGTCTGATCTCTTCTCCTCAGTAACTTATACAGAGGCTCCCATCTGC 1054  
 327 AlaSerValArgSerGlnLeuSerProSerSerLysValIleProGlyValProIleCys 346  
 1055 TTTCAGATAAACTGAGAAATTCAGATCTTCAATGAAATGAGAGTAAACGTTCTGTT 1114  
 347 PheGluValLysProGluGluSerSerAspAlaHisGluMetArgValLysArgSerIle 366  
 1115 ACAAGATAAAAGAGATCTGGAAGTGTTCCTACAGATGACCATCTGATATAGTA 1174  
 367 ThrArgIleLysLysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuVal 386  
 1175 TTTCGTGTACTTGGATGCCACTACCTTTTCCATGTGGTAACTGATTTTAAATGACAAT 1234  
 387 PheAlaValSerTrpMetProLeuHisValPheHisValThrAspPheAsnAspAsn 406  
 1235 CTTATTTCAAATAGGCATTTCAAGTGTGTGATTCATTTGTCATTTTCTTGGGCATGATG 1294  
 407 LeuIleSerAsnArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMet 426  
 1295 TCCTGTGCTTAATCCAAATCTATATGGGTTTCTTAATATGGATTAAGCTGATTTA 1354  
 427 SerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeu 446  
 1355 GTGTCCTCTATACACTGCTTCATATG 1381  
 447 ArgAlaLeuIleHisCysLeuHisMet 455

# RESULT 14

US-10-027-049-4  
 ; Sequence 4, Application US/10027049  
 ; Publication No. US2003002283A1  
 ; GENERAL INFORMATION:

; APPLICANT: Hu Ph.D., Yinghe  
 ; McCaleb Ph.D., Michael L.  
 ; Bloomquist Ph.D., Brian T.  
 ; Flores-Riveros Ph.D., Jaime R.

; Cornfield Ph.D., Linda J.  
 ; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
 ; Sequences  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
 ; STREET: 300 South Wacker Drive, 32nd Floor  
 ; CITY: Chicago  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA: US/10/027,049  
 ; FILING DATE: 08-Apr-1996  
 ; CLASSIFICATION: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Greenfield Ph.D., Michael S.  
 ; REGISTRATION NUMBER: 37,142  
 ; REFERENCE/DOCKET NUMBER: 96,149/WH 405  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312)715-1000  
 ; TELEFAX: (312)715-1234  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 445 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 ; US-10-027-049-4

Alignment Scores:  
 Pred. No.: 5,37e-193 Length: 445  
 Score: 2074.50 Matches: 394  
 Percent Similarity: 93.26% Conservative: 21  
 Best Local Similarity: 88.54% Mismatches: 29  
 Query Match: 83.65% Indels: 1  
 DB: 14 Gaps: 1

US-09-771-956-4 (1-1406) X US-10-027-049-4 (1-445)

Qy 47 ATGATTTAGACTGACGAGTATTTATACAGACACTTGCCACAGAGATTAATCTGCT 106  
 Db 1 MetGluPheLysLeuGluHisPheAsnLysThrPheValThrGluAsnThrAla 20  
 Qy 107 GCACCTCGGAATTCGATTTCCAGTCTGGGATGACTATAAAGCAGCTAGTAGACTTA 166  
 Db 21 AlaAlaArgAsnAlaAlaPheProAlaIlePheGluAspTyrArgGlySerValAspLeu 40  
 Qy 167 CAGTATTTCTGATTCGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGAATCTA 226  
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 Qy 227 CTTATTTTATGGCTCTCATGAAAAAGCCTAATCAGAGACTACGTAACCTTCCTCAT 286  
 Db 61 LeuIleLeuMetAlaValMetLysLysArgAsnGlnLysThrValAsnPheLeuIle 80  
 Qy 287 GGCAATCTGGCCCTTTTCTGATATCTTGGTGTGCTCTTTTGTCTCACCCTTTCACACTGACG 346  
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValPheCysSerProPheThrLeuThr 100  
 Qy 347 TCTGTCTTCTGATCAGTGGATGTTTGGCAAGTCATGTCGCAATATTATGCTTTTCTT 406  
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysAlaMetCysHisIleMetProPheLeu 120  
 Qy 407 CAATGTGTGTCAGTCTTTTGGTTTCAACTTTAATTTTAAATTTCAATTCCTCAGGTAT 466  
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140

QY 467 CATATGATAAAACATCCCATATCTAATAATTAAACAGCAAAACCATGGCTACTTCTGATA 526  
 Db 141 HisMetLleLysHisProLleSerAsnAsnLeuThrAlaAsnHisGlyTrpPheLeuLle 160  
 QY 527 GCTACTGCTGACACTAGGTTTCCCATCTGTTCTCCCTCCAGTGTTCACAGCTTT 586  
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
 QY 587 GTGGAACTTCAAGAAACATTTGGTTCAGCATTCGTGACGACGAGTATTTATGTTGAG 646  
 Db 181 ValGluLeuLysGluThrPheGlySerAlaLeuLeuSerLysTrpLeuCysValGlu 200  
 QY 647 TCATGCCCATCTGATTTCATACAGAAATTCGCTTACTCTCTTTATTCAGTTCAGTAT 706  
 Db 201 SerTrpProSerAspSerTrpArgIleAlaPheThrIleSerLeuLeuValGlnTrp 220  
 QY 707 ATTCTGCCCTTACTGTTCTACTGTAAGTCTATCAAGTGTCTGACAGAGTATAAGCTGT 766  
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
 QY 767 GGATTGTCCAAAGAAACACAGACTTCAAGAAATGAGATGATCAACTTAACTCTTCAT 826  
 Db 241 GlyLeuSerHisLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuGln 260  
 QY 827 CCATCAAAAGAGTGGGCTCAGTGAACTCTCTGGCAGCCATAAATGGAGTATTATCA 886  
 Db 261 ProSerLysLysSerArgAsnGlnAlaLysThrProSerThrGlnLysTrpSerTrpSer 280  
 QY 887 TTCATCAAAACACAGAGAGATATAGCAAGAGACAGCATGTGTACCTGCTCCCA 946  
 Db 281 PheIleArgLysHisArgArgTrpSerLysLysThrAlaCysValLeuProAlaPro 300  
 QY 947 GAAAGACCTTCTCAAGAAACCATCCAGATCTCCAGAAATCTTCAGAAACTTTGGCTGTGA 1006  
 Db 301 AlaGlyProSerGlnGlyLysHisLeuAlaVal--ProGluAsnProAlaSerValArg 319  
 QY 1007 AGTCAGCTCTTCTCATCAGTAAGTTCTACAGGGTCCCTCCCTGCTTGTAGATAAAA 1066  
 Db 320 SerGlnLeuSerProSerSerLysValIleProGlyValProIleCysPheGluValLys 339  
 QY 1067 CCTGAAGAAATTCAGATGTTTCATGATTTGAGAGTAAACCTCTGTTTACAGAAATAAAA 1126  
 Db 340 ProGluGluSerSerAspAlaHisGluMetArgValLysArgSerIleThrArgIleLys 359  
 QY 1127 AAGAGATCTGAGAGTCTTCTACAGACTGACCATGATGATGATGATGATGATGATGATG 1186  
 Db 360 LysArgSerArgSerValPheTrpArgLeuThrIleLeuIleLeuValPheAlaValSer 379  
 QY 1187 TGGATGCCACTACACTTTTCCATGTGTGTAACATGATTTTATGACATCTTATTTCAAA 1246  
 Db 380 TrpMetProLeuHisValPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 399  
 QY 1247 AGGCAATTCAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1306  
 Db 400 ArgHisPheLysLeuValTrpCysIleCysHisLeuLeuGlyMetMetSerCysLeu 419  
 QY 1307 AATCAATCTATATGCTGTTCTTAAATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1366  
 Db 420 AsnProIleLeuTrpGlyPheLeuAsnAsnGlyIleLysAlaAspLeuArgAlaLeuIle 439  
 QY 1367 CACTGTCTTCATATG 1381  
 Db 440 HisCysLeuHisMet 444

RESULT 15

US-10-027-049-2  
 ; Sequence 2, Application US/10027049  
 ; Publication No. US2003002283A1

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;  
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 ; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
 ; Sequences

;  
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;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA: US/10/027,049  
 ; FILING DATE: 08-Apr-1996  
 ; CLASSIFICATION: <Unknown>  
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 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 445 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 ; US-10-027-049-2

Alignment Scores:

Pred. No.: 2,588-192 Length: 445  
 Score: 2067.50 Matches: 393  
 Percent Similarity: 93.03% Conservative: 21  
 Best Local Similarity: 88.31% Mismatches: 30  
 Query Match: 83.37% Indels: 1  
 DB: 14 Gaps: 1

US-09-771-956-4 (1-1406) X US-10-027-049-2 (1-445)

QY 47 ATGGATTATAGACTCGACGAGTATTATAACAGACACTTGCACAGAGAAATAACTGCT 106  
 Db 1 MetGluPheLysLeuGluHisPheAsnLysThrPheValThrGluAsnAsnThrAla 20  
 QY 107 GCACCTCGGAATTCGATTCCCACTCTGGAGTACTATAAAGCAGGTAGATCACTTA 166  
 Db 21 AlaAlaArgAsnAlaAlaPheProAlaTrpGluAspTrpArgGlySerValAspLeu 40  
 QY 167 CAGTATTTTCGATTTGGGCTCTATACATTTGTAAGTCTTCTTGGGCTTTATGGGAACTA 226  
 Db 41 GlnTrpPheLeuIleGlyLeuTrpPheValSerLeuLeuGlyPheMetGlyAsnLeu 60  
 QY 227 CTTATTTTAAAGTCTCATGAAAGGCTATCAAGAGACTAGCTAAAGTCTCTCATATA 286  
 Db 61 ProIleLeuMetAlaValMetLysLysArgAsnGlnLysThrValAspPheLeuIle 80  
 QY 287 GGCAATCTGGCCTTTTCTCATATCTTGGTGTGTGCTGTTTGTCTACCTTTTCACACTGAC 346  
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100  
 QY 347 TCTGCTTCTGCGATCAGTGGATGTTTGGCAAGTCATGTGCCATATATGCTTTTCTT 406  
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysAlaMetCysHisIleMetProPheLeu 120  
 QY 407 CAATGTGTCTCAGTTTGTGTTTCAACTTTAATTTTAAATCAATTCGCAATTCGAGGTAT 466

Db 121 GlnCysValSerValLeuValSerThrLeuLeuLeuSerIleAlaIleValArgTyr 140  
QY 467 CATATGATAAAACATCCCATATCTAATAATTAAACAGCAACCATGCTACTTTCTGATA 526  
Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160  
QY 527 GCTACTGCTGGACACATAGGTTTGGCCATCTGTTCTCCCTTCCAGTCTTTCACAGTCT 586  
Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180  
QY 587 GTGGAACCTTCAAGAAACATTTGGTTTCAGCATTTGTCAGCAGCAGGATTATTTATGTTGAG 646  
Db 181 ValGluLeuLysGluThrPheGlySerAlaLeuLeuSerSerLysTyrLeuCysValGlu 200  
QY 647 TCATGGCATTCTGATTCATACAGAAATTCCTTTACTATCTCTTTATTGCTAGTTCAGTAT 706  
Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220  
QY 707 ATTCGCTCCCTTAGTTCTCTACTGTAAGTCATACAAAGTGTCTGCAGAACTATAAGCTGT 766  
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240  
QY 767 GGATTGTCCAAACAGAAACAGACTTCAAGAAATGAGATGATCAACTTAACCTTTCAT 826  
Db 241 GlyLeuSerHisLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuGln 260  
QY 827 CCATCCAAAAGAGTGGCCCTCAGCTGAAACTCTCTGGCAGCCATAATGGAGTTATTC 886  
Db 261 ProSerLysLysSerArgAsnGlnAlaLysThrProSerThrGlnLysTrpSerTyrSer 280  
QY 887 TTCTATCAAAAACACAGAAAGATATAGCAAGAGACAGCATGTGTGTACCTGTCTCCA 946  
Db 281 PheIleArgLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300  
QY 947 GAAAGACCTTCTCAAGAGAACCTCCAGATACTCCAGAAACTTTGGCTCTGTGAAGA 1006  
Db 301 AlaGlyProSerGlnGlyLysHisLeuAlaVal---ProGluAsnProAlaSerValArg 319  
QY 1007 AGTCAGTCTCTTCATCCAGTAAGTTCATACAGGGGTCCCACTTCTCTTTGAGATAAAA 1066  
Db 320 SerGlnLeuSerProSerSerLysValIleProGlyValProlleCysPheGluValLys 339  
QY 1067 CCTGAAGAAAATTCAGATGTTTCATGAATTGAGAGTAAACGTTCTGTTCACAGAAATAAA 1126  
Db 340 ProGluGluSerSerAspAlaHisGluMetArgValLysArgSerIleThrArgIleLys 359  
QY 1127 AAGAGATCTCGAAGTGTCTTACAGACTGACCATGATGATATTAGTATTGCTGTAGT 1186  
Db 360 LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuValPheAlaValSer 379  
QY 1187 TGGATGCCACATACACCTTTTCCATGTGTGAATTTAATGACAATCTTATTTCAAAT 1246  
Db 380 TrpMetProLeuHisValPheHisValThrAspPheAsnAspAsnLeuIleSerAsn 399  
QY 1247 AGGCATTTCAAGTTGGTGTATTGCAATTTGTCATTTGTTGGCATGATGCTGTGTCTT 1306  
Db 400 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLeu 419  
QY 1307 AATCCAAATCTATATGGGTTTCTTAATAATGGGATTAAAGCTGATTAGTGTCCCTTATA 1366  
Db 420 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuArgAlaLeuIle 439  
QY 1367 CACTGTCTTCATATG 1381  
Db 440 HisCysLeuHisMet 444

Search completed: October 21, 2004, 12:07:40  
Job time : 209 secs

